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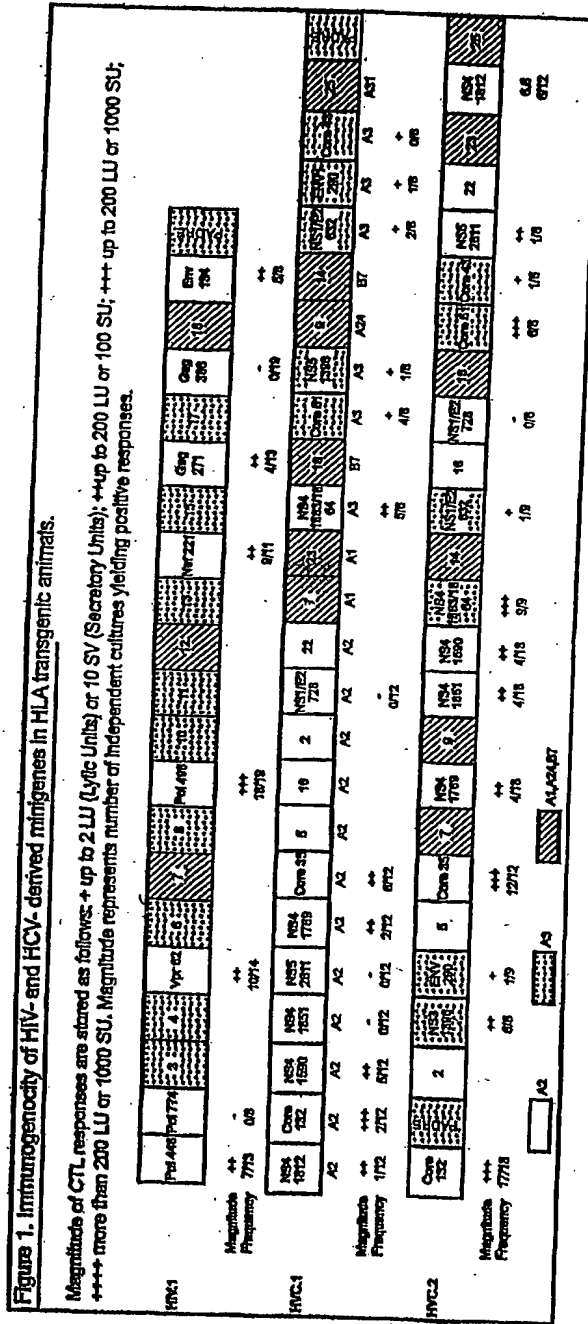
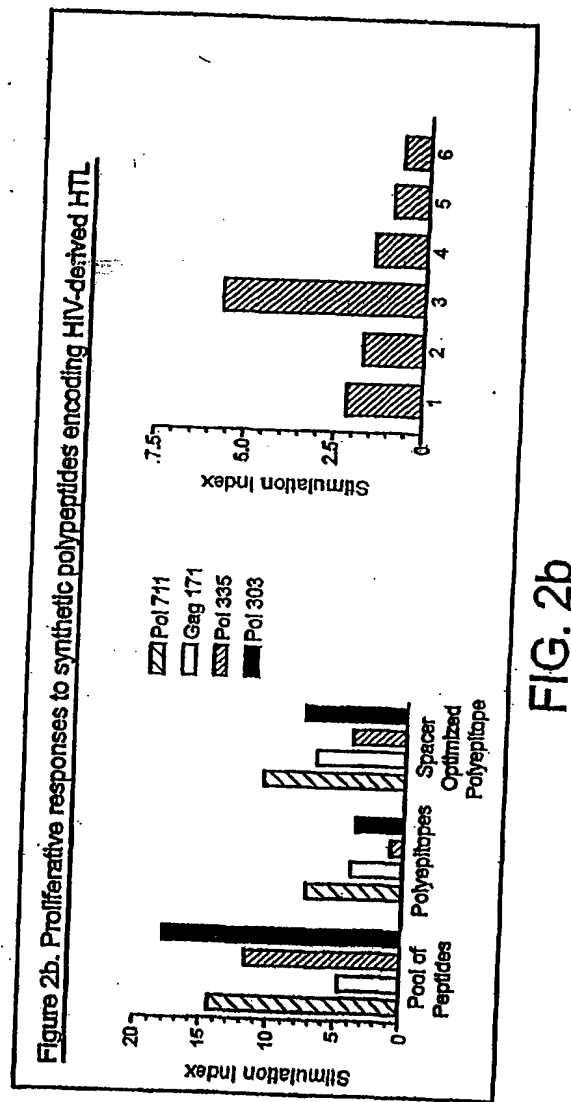
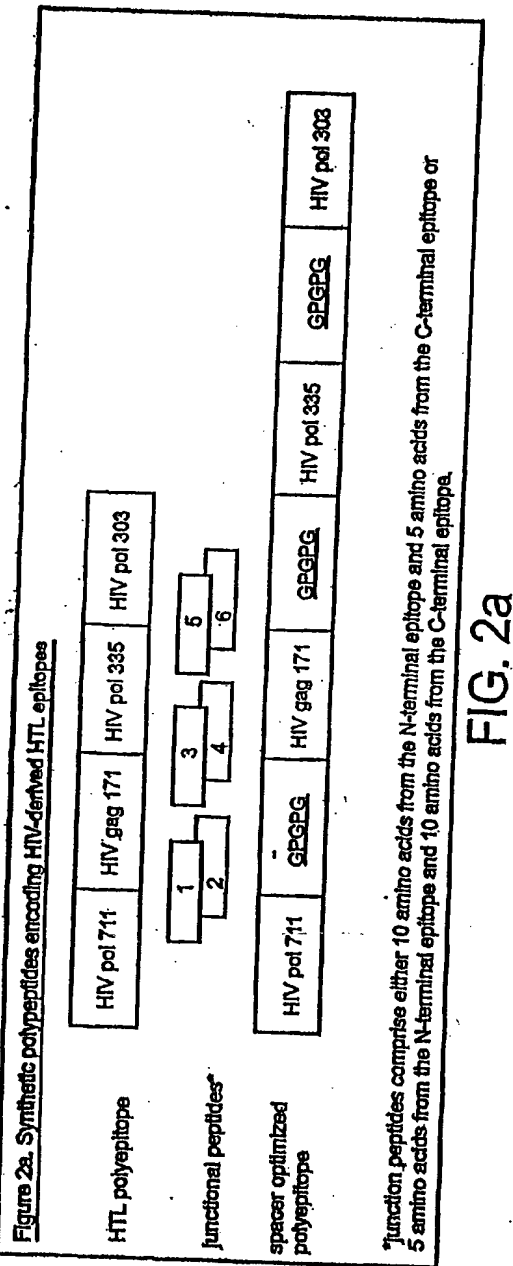
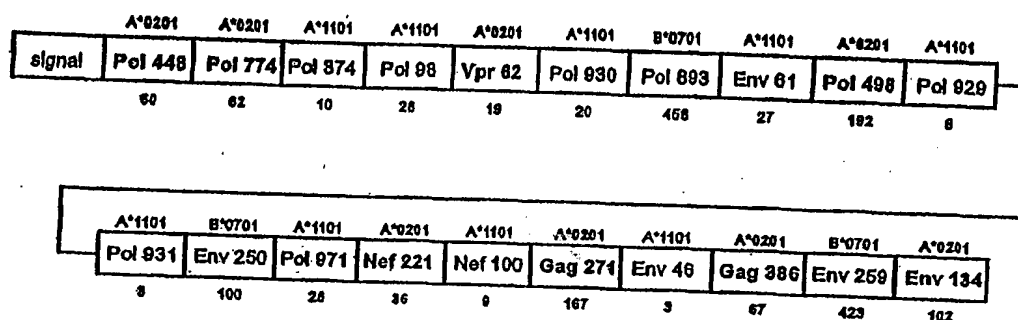


FIG. 1

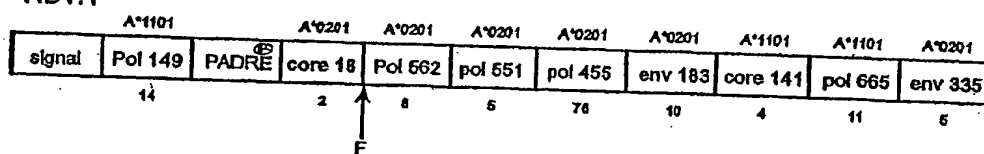


a : HIV-FT

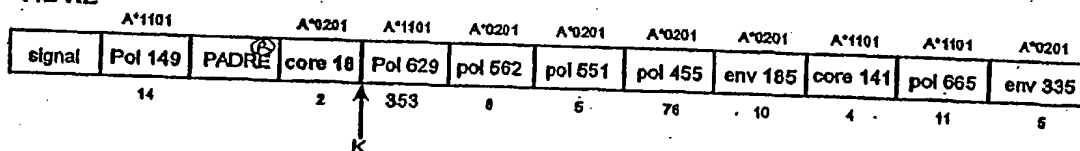


b : HBV-specific multi-epitope constructs

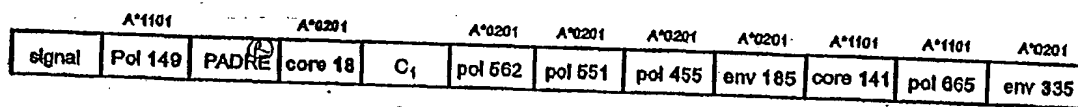
HBV.1



HBV.2



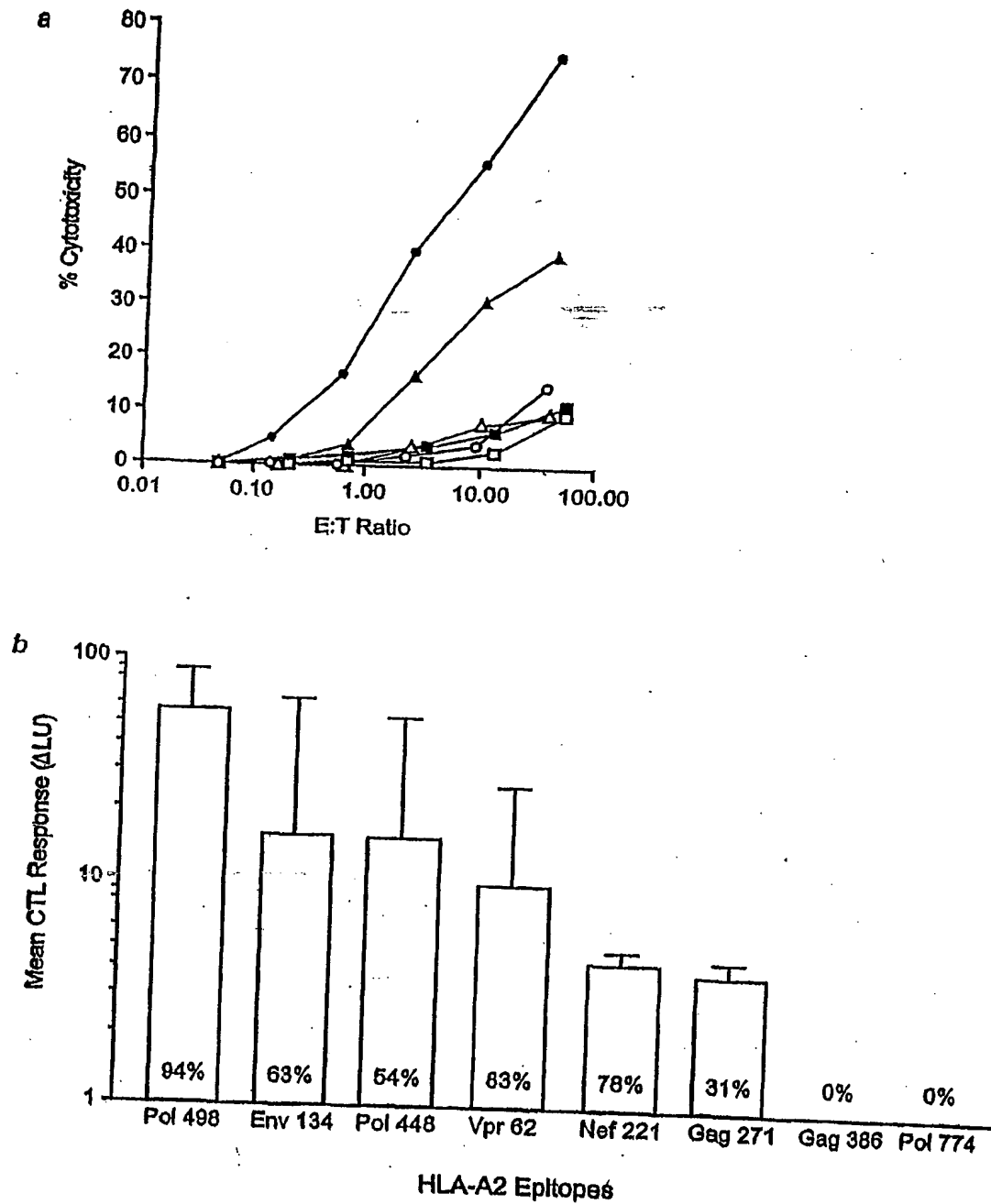
HBV.1X



C<sub>1</sub> = either W, Y, L, K, R, C, N or G

FIG. 3

Figure 4



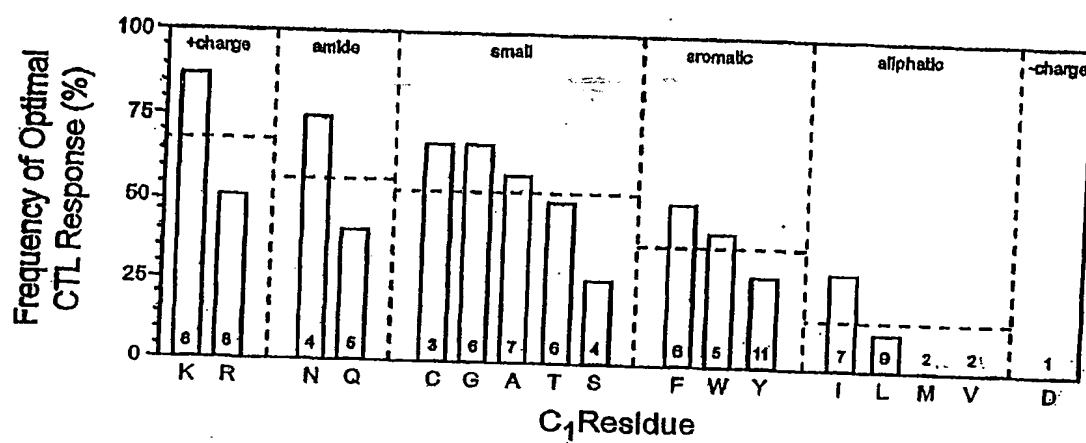
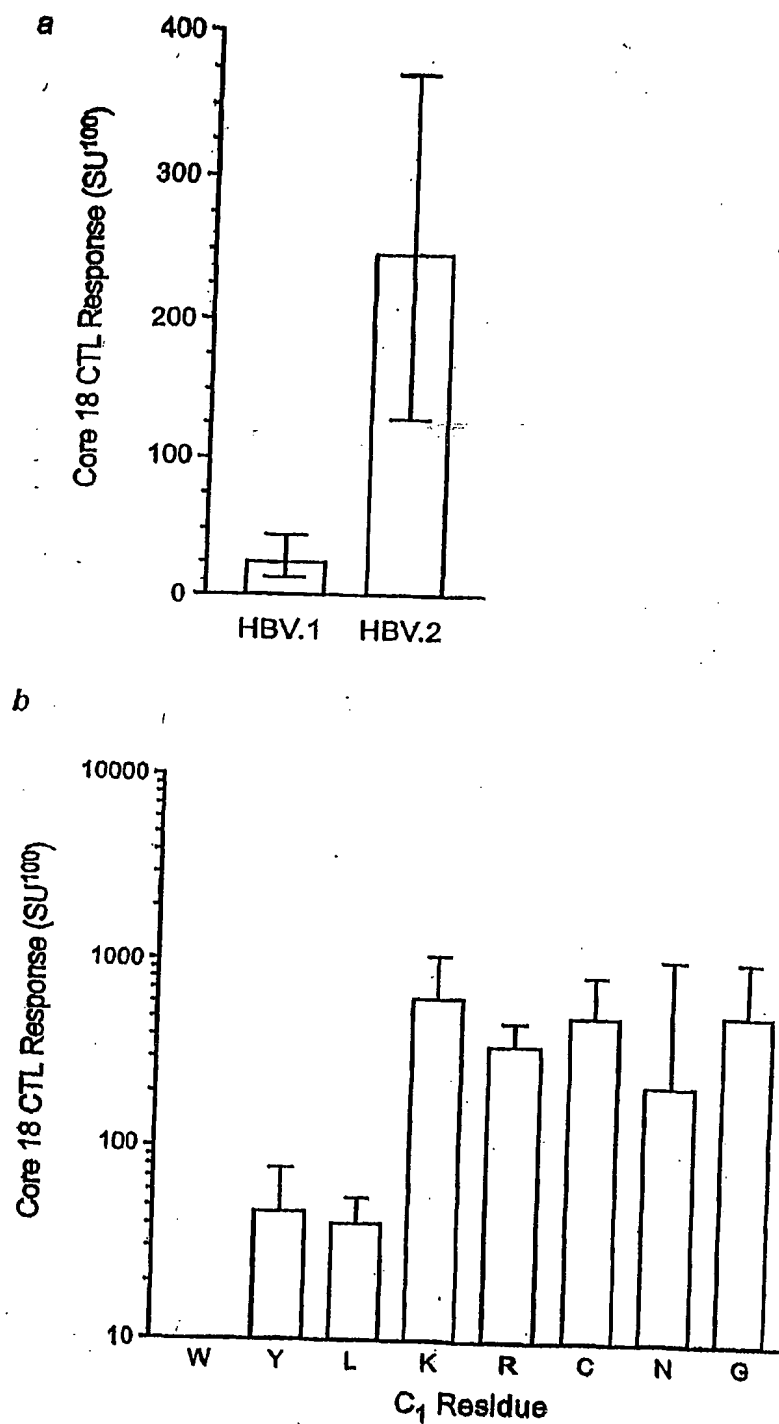


FIG. 5



**FIG. 6**

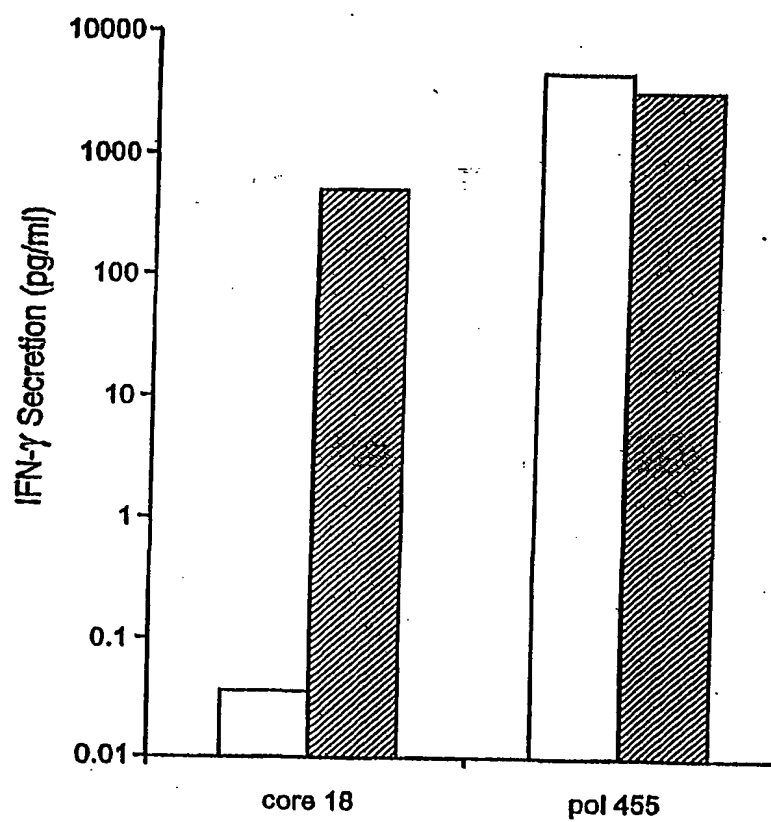


FIG. 7



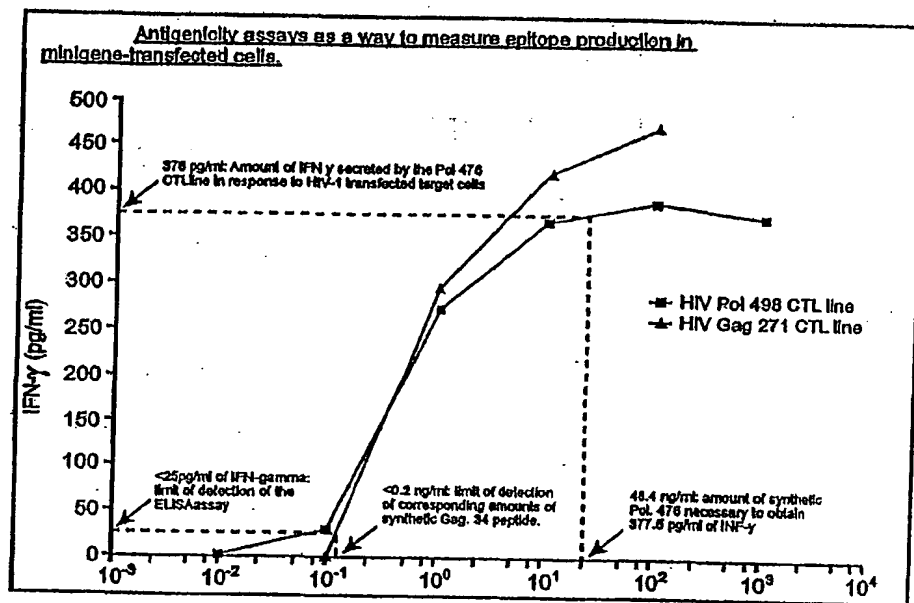
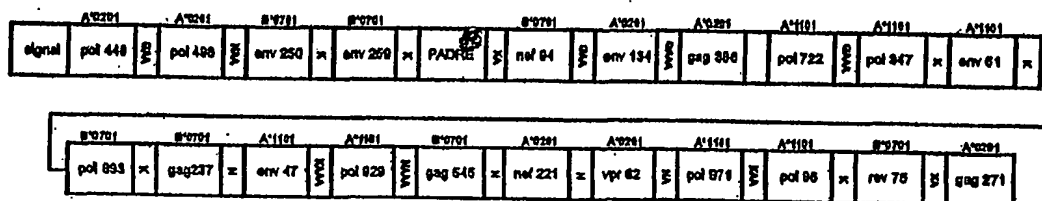
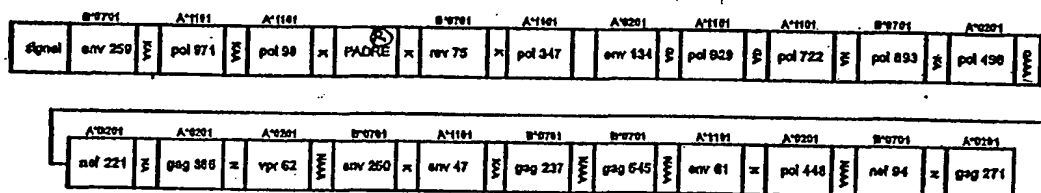


FIG. 8

# HIV-TT



# HIV-DG



# HIV-TC

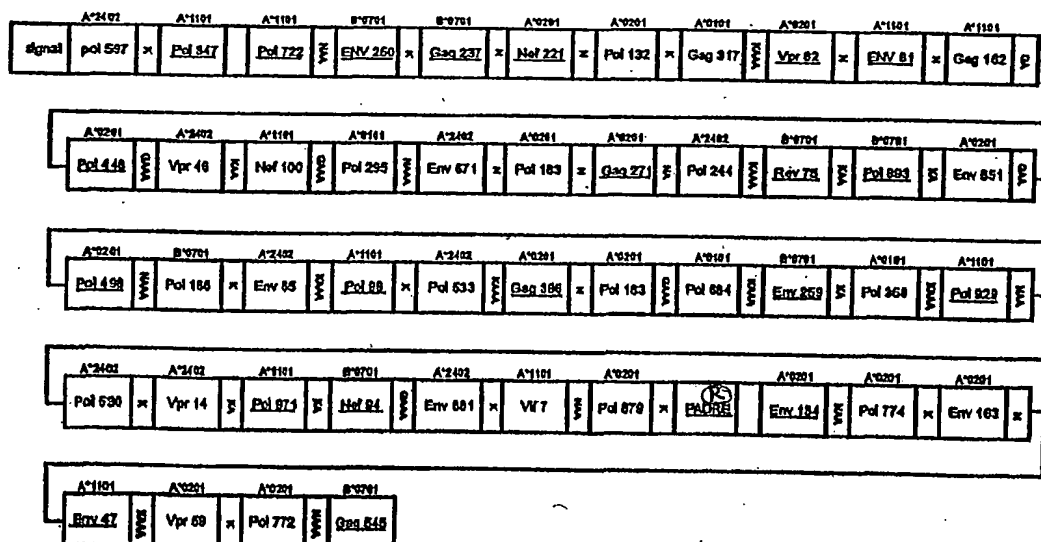


FIG. 9

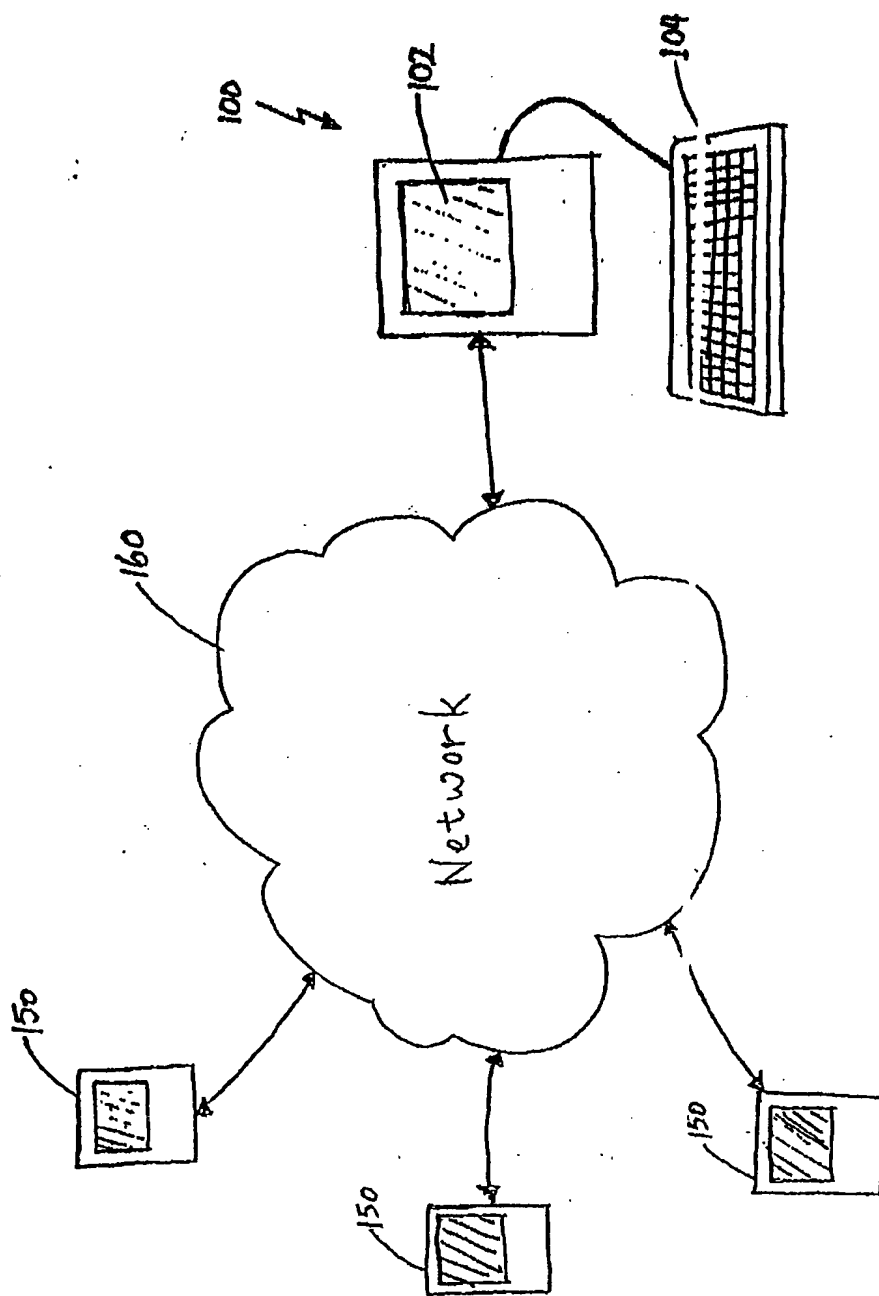


FIGURE 10

200  
⚡

Sequence	Length	Code
VLAHAMSQV	9	A
ILKEPVHGV	9	B
TLNFPISPI	9	C
SLLNATDIAV	10	D
QMAVFTHNFK	10	E
VTVYYGVFVWK	11	F
FPVRPQVPL	9	G
YPLASLRSLF	10	H
VTYQYMDDLY	10	I
IYQEPFKNL	9	J
IWGCŞGKLI	9	K

202

AA	O+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LMV)  
 XXXX(FY)XXX(LIMV)  
 XXXXNXXX(LIMV)  
 XXXXNXXXX(LIMV)  
 X(LM)XXXXXXV  
 X(LM)XXXXXXXXV  
 X(LMVT)XXXXXX(KRY)  
 X(LMVT)XXXXXX(KRY)  
 XPXXXXXX(LIMVF)  
 XPXXXXXX(LIMVF)

206

FIGURE 11A

**MaxInsertions={enter value here} 208**  
**OutputToScreen=yes/no 210**  
**OutputToFile=yes/no 212**  
**MinimumAccepted={enter value here} 214**  
**MaxDuplicateFunctionValues={enter value here} 216**  
**MaxSearchTime (min.)={enter value here} 218**  
**Exhaustive=yes/no 220**  
**NumStochasticProbes={enter value here} 222**  
**MaxHitsPerProbe={enter value here} 224**  
**RandomProbeStart=yes/no 226**

**FIGURE 11B**

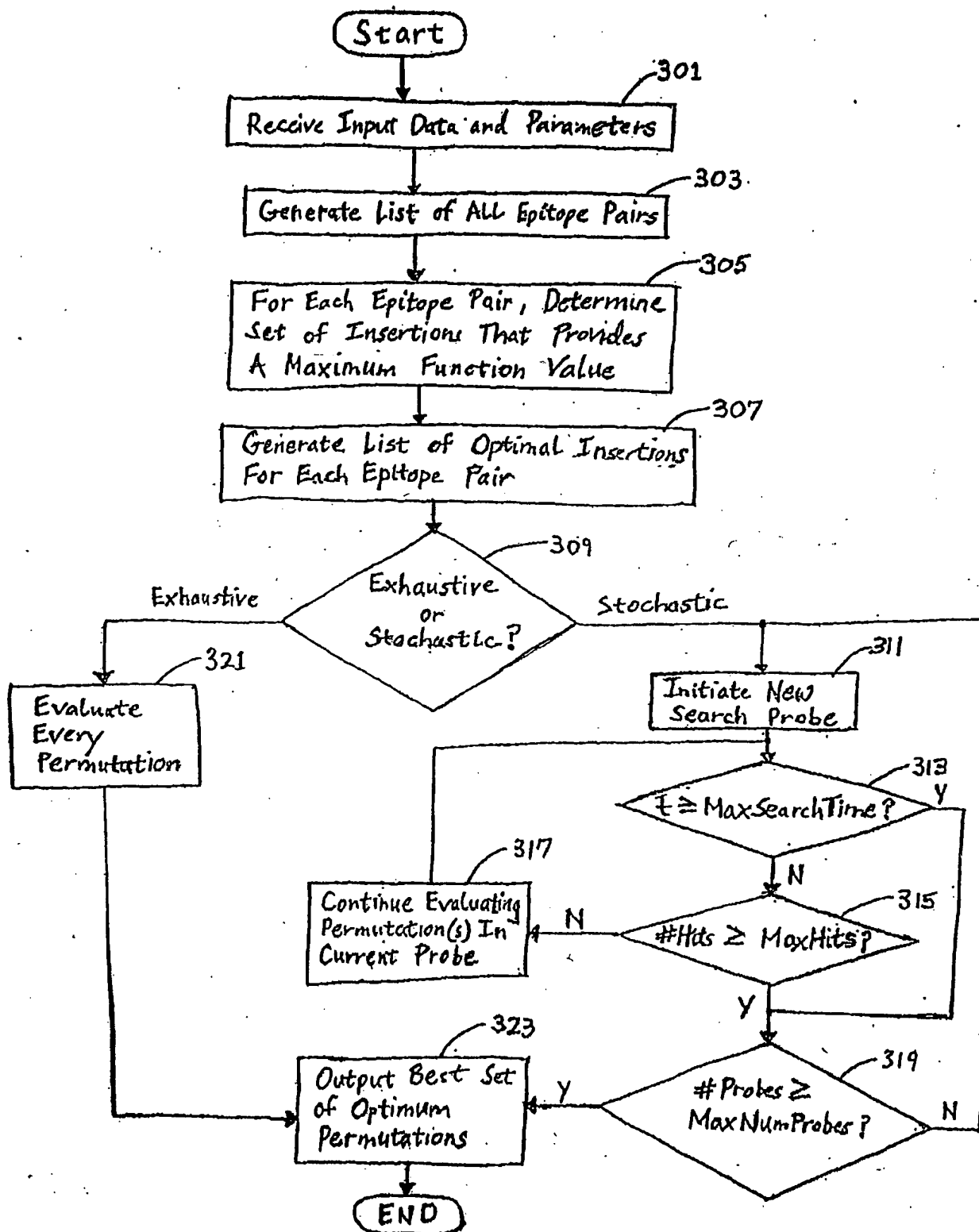


FIGURE 12

Junctional Analyzer run on Saturday, February 26, 2000 09:08:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.88
K	0.84	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV)
2	XXXX(FY)XXX(LIMV)
3	XXXXNXXX(LIMV)
4	XXXXNXXXX(LIMV)
5	X(LM)XXXXXXV
6	X(LM)XXXXXXXV
7	X(LMVT)XXXXXX(KRY)
8	X(LMVT)XXXXXXX(KRY)
9	XPXXXXXX(LIMVF)
10	XPXXXXXXX(LIMVF)

206

Code	Peptide	Length
A	VLAEMSQV	9
B	ILKEPVHGV	9
C	TLNFPISPI	9
D	SLLNATDIIV	10
E	QMAVFIHNFK	10
F	VTVYYGVPVWK	11
G	FPVRPQVPL	9
H	YPLASLRSLF	10
I	VIIQYMDDLY	10
J	IYQEPFKNL	9
K	IWGCSGKLI	9

202

MaxInsertions = 4 (208)

FIGURE 13A

OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 60

SearchTime = 6

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	G			R	H	2.00	1.57	3.14	0	6.28
A	C				I	1.80	1.33	2.66	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C		A	G	K	2.00	1.57	3.14	0	6.28
B	C	A	A	R	A	2.00	1.33	2.66	0	5.32
B	C	A	A	R	C	2.00	1.57	3.14	0	6.28
B	C	A	A	R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C	A	A	R	F	2.00	1.33	2.66	1	2.66
B	C		A	R	G	2.00	1.57	3.14	1	3.14
B	C	A	A	R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C			R	A	2.00	1.57	3.14	1	3.14
C	C			L	B	2.00	1.57	3.14	1	3.14
C	C	A		R	D	2.00	2.20	4.40	1	4.40
C	C			R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C	A		R	H	2.00	1.57	3.14	1	3.14
C	C	A		R	I	2.00	1.57	3.14	0	6.28
C	C	A	A	R	J	2.00	1.57	3.14	1	3.14
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28
						2.00	1.57	3.14	0	6.28

FIGURE 13B



Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	C			L	F	1.80	1.33	2.89	0	4.79
D	C			L	G	2.00	1.57	3.14	0	6.28
D	C	A	A	R	H	2.00	1.33	2.66	0	5.32
D	C	A		L	I	2.00	2.20	4.40	1	4.40
D	C	A		G	J	2.00	1.33	2.66	0	5.32
D	C	A	A	R	K	2.00	1.57	3.14	0	6.28
D	C	A	A	L	A	2.00	2.20	4.40	0	8.80
D	C	A	A	L	B	2.00	2.20	4.40	0	8.80
D	C	A	A	L	C	2.00	2.20	4.40	0	8.80
D	C	A	A	L	D	2.00	2.20	4.40	0	8.80
D	C	A	A	L	F	2.00	1.57	3.14	0	6.28
D	C	A	A	L	G	2.00	1.57	3.14	0	6.28
D	C	A	A	L	H	2.00	1.57	3.14	0	6.28
D	C	A	A	L	I	2.00	2.20	4.40	0	8.80
D	C	A		R	J	2.00	1.57	3.14	0	6.28
D	C	A		R	K	2.00	1.57	3.14	0	6.28
D	C	A		L	A	2.00	1.57	3.14	0	6.28
D	C	A	A	G	B	2.20	2.20	4.84	1	4.84
D	C	A	A	G	C	2.20	1.33	2.93	1	2.93
D	C	A	A	G	D	2.20	1.33	2.93	0	5.85
D	C	A	A	G	E	2.20	1.33	2.93	0	5.85
D	C	A		G	G	2.20	1.33	2.93	1	2.93
D	C	A		G	H	2.20	1.33	2.93	1	2.93
D	C	A		G	I	2.20	1.33	2.93	1	2.93
D	C	A		G	J	2.20	1.57	3.45	1	3.45
D	C	A		R	K	2.20	1.57	3.45	0	6.91
D	C	A		R	A	2.00	1.57	3.14	1	3.14
D	C	A		R	B	2.00	1.57	3.14	2	1.57
D	C	A		R	C	2.00	1.57	3.14	1	3.14
D	C	A		R	D	2.00	2.20	4.40	1	4.40
D	C	A		L	E	2.00	1.57	3.14	2	1.57
D	C	A		L	F	2.00	2.20	4.40	4	1.10
D	C	A	A	R	H	2.00	1.33	2.66	0	5.32
D	C	A	A	R	I	2.00	1.57	3.14	2	1.57
D	C	A	A	R	J	2.00	1.57	3.14	1	3.14
D	C	A	A	R	K	2.00	1.57	3.14	0	6.28
D	C	A	A	G	A	2.00	1.33	2.66	0	5.32
D	C	A	A	G	B	2.00	1.33	2.66	1	2.66
D	C	A	A	G	C	2.00	1.33	2.66	0	5.32
D	C	A	A	G	D	2.00	1.33	2.66	0	5.32
D	C	A	A	G	E	2.00	1.33	2.66	0	5.32
D	C	A	A	G	F	2.00	1.33	2.66	1	2.66
D	C	A	A	G	G	2.00	1.57	3.14	1	3.14
D	C	A	A	G	I	2.00	1.33	2.66	1	2.66
D	C	A	A	G	J	2.00	1.33	2.66	1	2.66
D	C	A	A	G	K	2.00	1.33	2.66	0	5.32

FIGURE 13C

Code 1	I1	I2	I3	I4	Code 2	C	N	O+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.93	2.93	0	5.85
I	K	A	A	G	B	2.20	1.93	2.93	1	2.93
I	K	A		G	C	2.20	1.93	2.93	0	5.85
I	K	A		G	D	2.20	1.93	2.93	0	5.85
I	K	A	A	G	E	2.20	1.93	2.93	0	5.85
I	K	A	A	G	F	2.20	1.93	2.93	1	2.93
I	K		A	R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.93	2.93	0	5.85
I	K	A	A	G	J	2.20	1.93	2.93	1	2.93
J	K	A	A	R	K	2.20	1.93	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K		A	R	F	2.20	1.57	3.45	2	1.73
J	K		A	R	G	2.20	1.57	3.45	1	3.45
J	K	A	A	R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
K	K		A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K	A	A	L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K		A	L	F	2.20	1.57	3.45	1	3.45
K	K			R	G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			R	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D

CTL responses induced by EP HIV-1090 relative to individual peptides in IFA

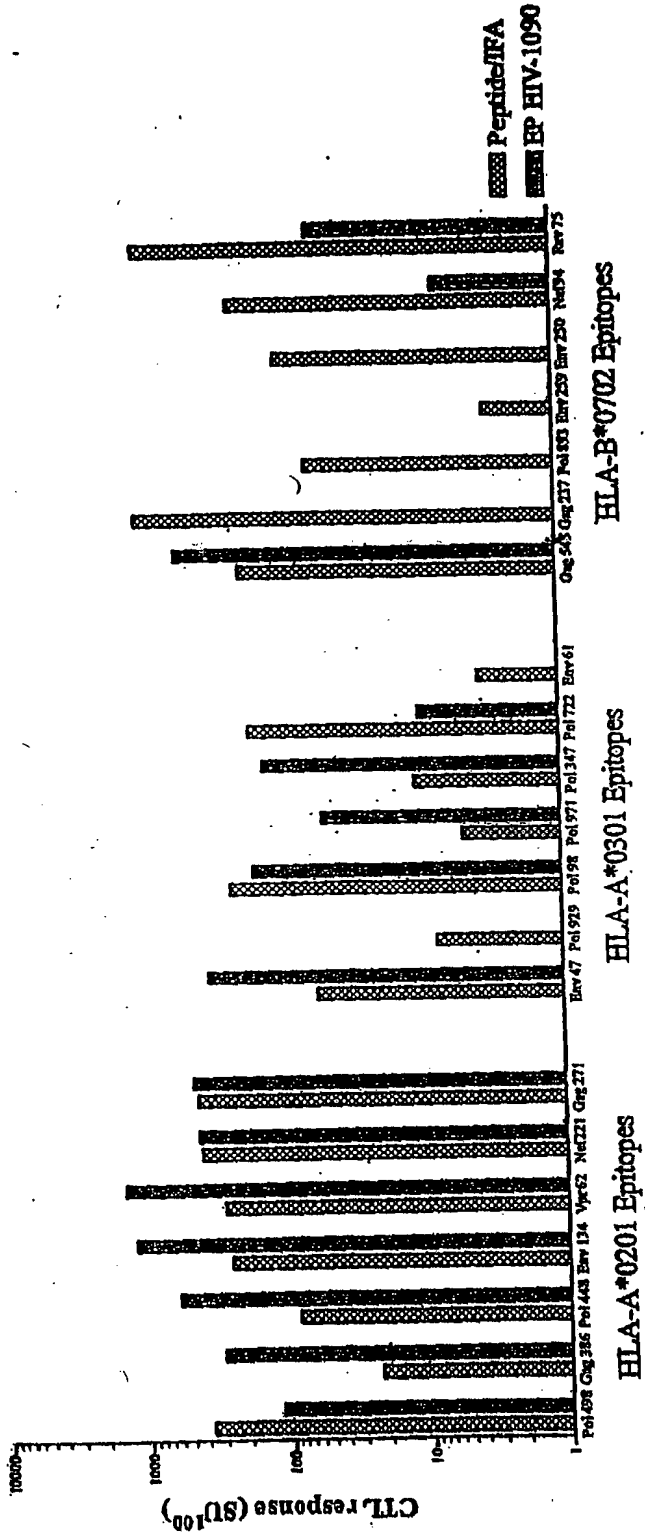
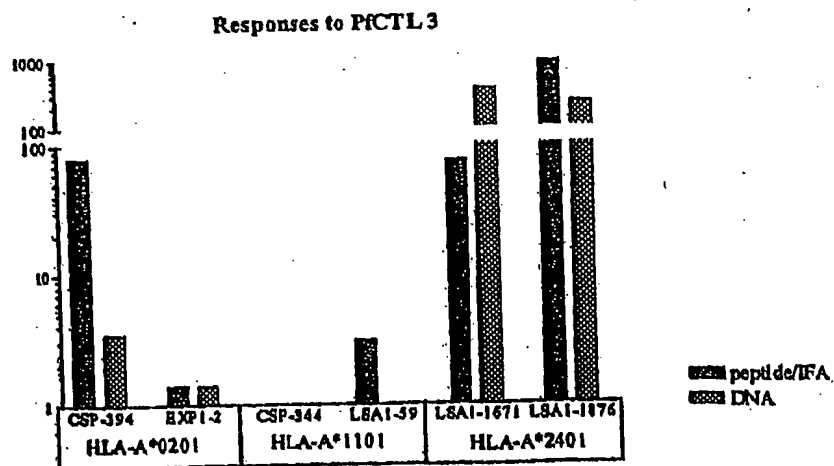
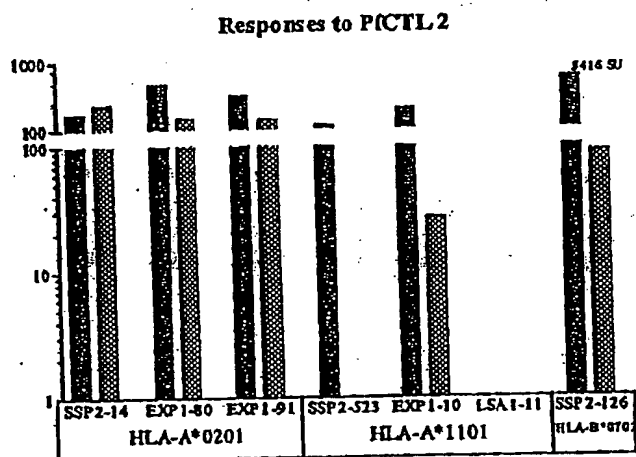
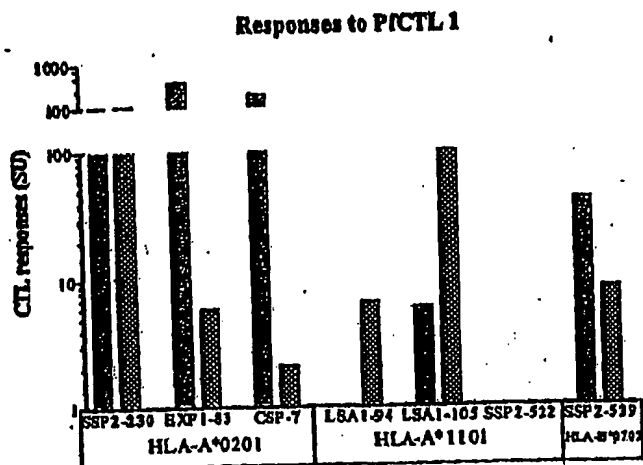


FIGURE 14A



**FIGURE 14B**

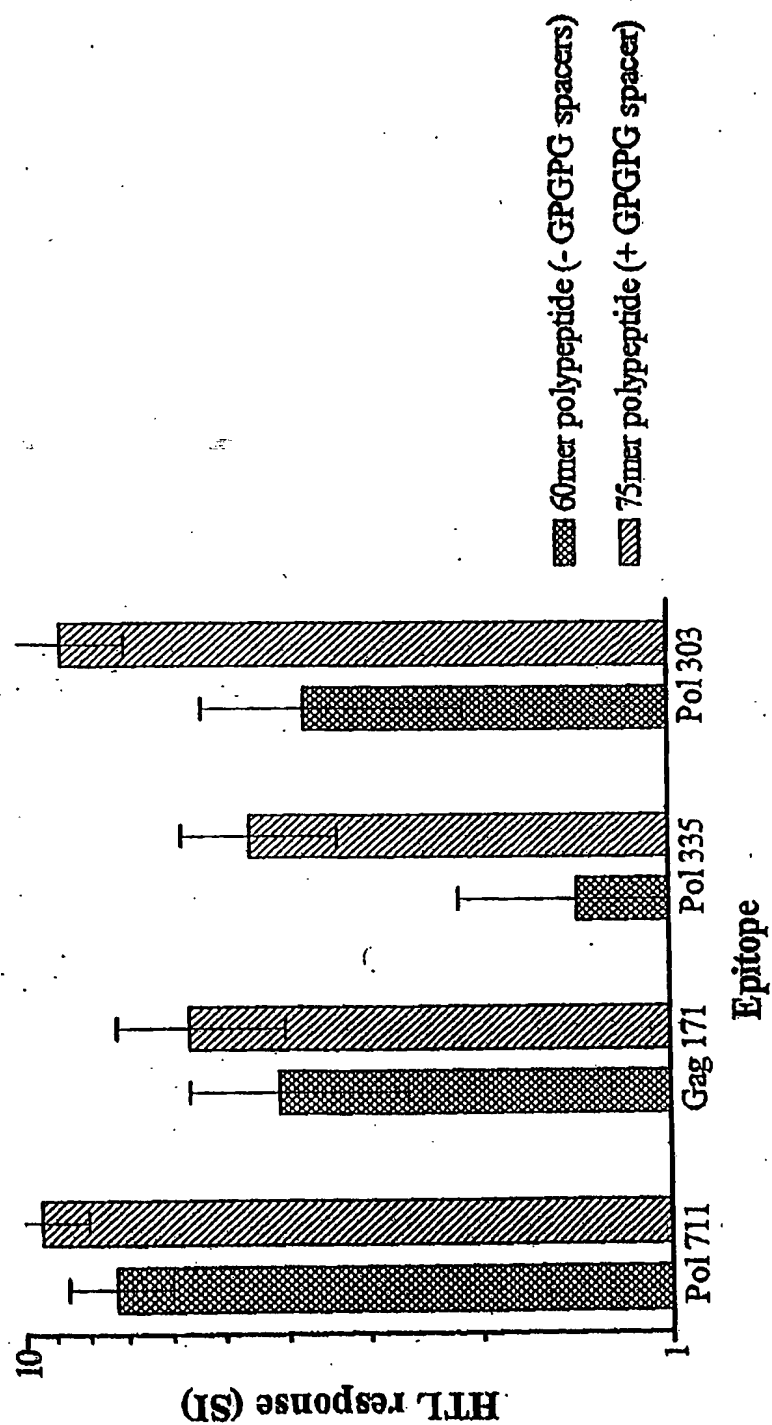


FIGURE 15

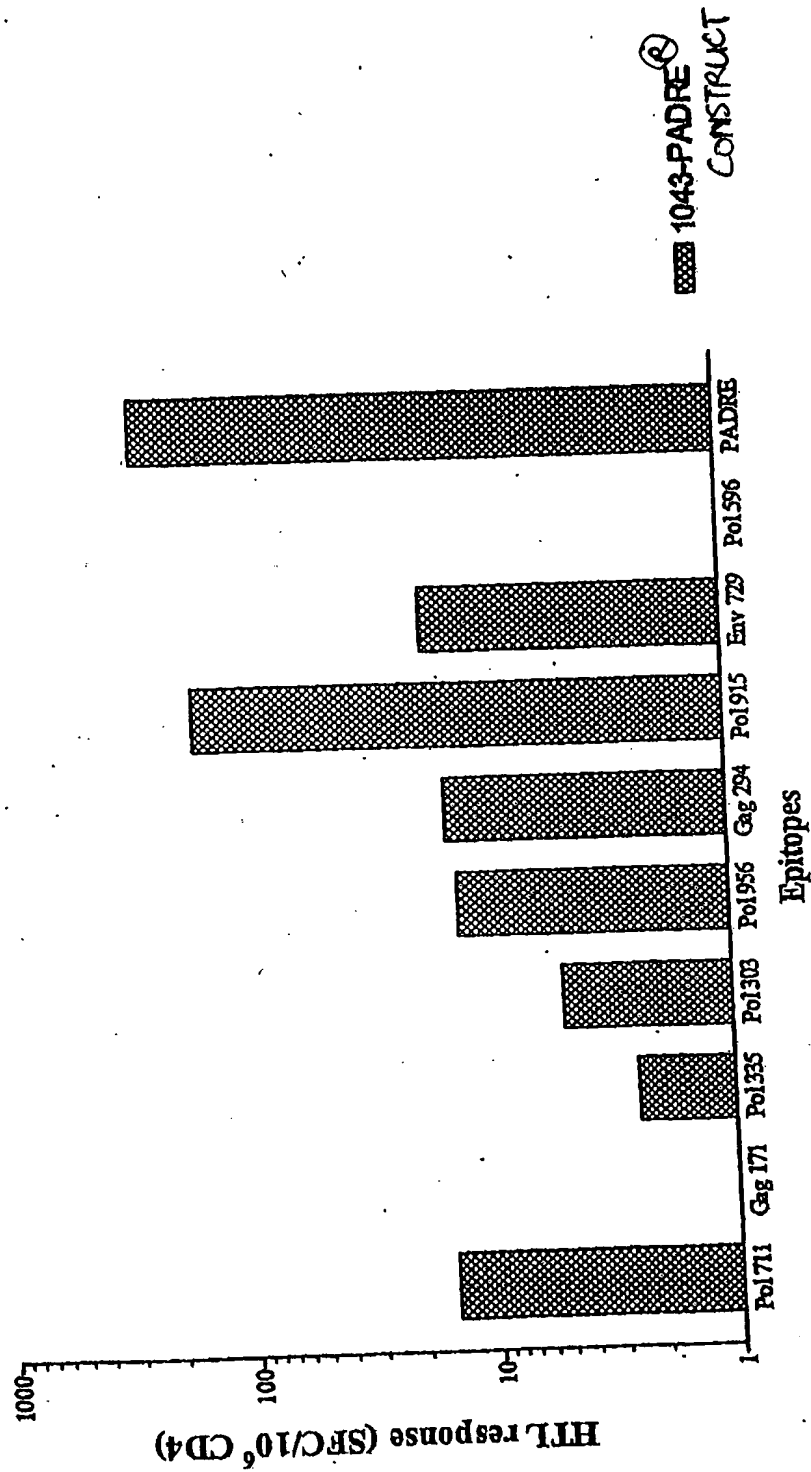


FIGURE 16

HIV 75mer

Pol 711	Qng 171	Pol 335	Pol 303
---------	---------	---------	---------

EP HIV-1043

Pol 711/712	Pol 956	Pol 596	Vpr 31	Env 729	Qng 294/295	Qng 171	Env 566	Pol 674	Pol 915	Pol 335	Pol 674	Pol 723	Pol 619	Pol 989	Pol 303
-------------	---------	---------	--------	---------	-------------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------

EP HIV-1043

Pol 711/712	Pol 956	Pol 596	Vpr 31	Env 729	Qng 294/295	Qng 171	Env 566	Pol 674	Pol 915	Pol 335	Pol 674	Pol 723	Pol 619	Pol 989	Pol 303	Pol 619
-------------	---------	---------	--------	---------	-------------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------

FIGURE 17

**EP-HIV-1090**

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKPIHYCAPA  
KAKFVAAWTLKAAAKAFVVRPQVPLGAAKLTPLCVTLGAAAVLABAMSQVKVYLAWVPAHKG  
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVVKHPVHAGPIANVTVYYGVVWKKAAAQMA  
VFIHNFKNAAAYPLASLRSFLNLTGWCFLNRLQQLLFINAKIQNFRVYYRKA AVTIKIGGQLKK  
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAAAGCTGGTGGGCAAACTCAACTGGGCGGAGCTGCAATCCTGAAGGAGCCCGTCCACGG  
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCATTACTGTGC  
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGGACCCCTCAAGGCCGCTGCAAAAGCCTTCCAGT  
GAGGCCCCAGGTGCTCTGGGCGCCGCTAAACTCAGACCACTGTGCGTCACTCTGGGAGCCGC  
TGCAGTGTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCGCCACAA  
GGGGGCCGCTGCAGCATCTTTCAGTCTAGCATGACCAAGAAAACAACTCTGTTCTGTGCTC  
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC  
CGGAACCTATTGCTAACGTGAACGTGTACTATGGGGTCCAGTGTGGAAGAAAGCCCGTGCACA  
GATGGCCGTGTTTATTACAAATTTCAAAAACGCCGCTGCATACCCCTCGCCAGCCTGAGATC  
CCTCTTCAACCTGACATTGGGCTGGTGTCTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTT  
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT  
GGCGGACAACTGAAGAAAGTGCCCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC  
CCCTATCCCACTCTGA

**HIV-CPT**

MGMQVQIQSLFLLLLWVPGSRGPIHYCAPAKAAKIQNFRVYYRKA AVTIKIGGQLKKAKFVAAW  
TLKAAAKVPLQLPPLKAIFQSSMTKKTLPCLVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN  
PQSQGVVKAILEKPVHGVGAAALTFGWCFKLNVLAEAMSQVNRILQQLLFINAAACPKVSFEPI  
KVTVYYGVVWKKAAHPVHAGPIANAAAYPLASLRSFLNAAATTLFCASDAKNKLVGKLNWAN  
AAAFVVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAATCCCCATTCACTACTGCGCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT  
TACAGAAAAGGCTGCAGTCACCATTAAAATCGGCGGACAACTGAAGAAAGCCAAAGTTTGTGGC  
CGCTTGGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGCTCCGCCCTCTGAAGGCCATCTT  
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGGCCAGATGGCTGT  
GTTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCGCACACAAGAACGC  
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG  
GGTGGGCGCCGCTGCACTCACTTTCGGATGGTGTCTTAAACTGAACGCCGTGCTGGCTGAAGC  
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCATTAACGCCGCTGCATGTCTTAA  
GGTGTCTCTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCGGTGTGGAAGAAAGCCGC  
TCATCCTGTCCACGACGGCCCAATCGCCAACGCCGCTGCATATCCCTCGCCTCTCTGCGCAG  
CCTGTTTAAACGCCGCTGCAACAACCCCTCTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG  
AAAGCTGAACCTGGGCCAACGACAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC  
TAACAATCCCCCTATCCCACTGTGA

**FIGURE 18A**



HIV-ET  
MQVQIQSLFLLLLWVPGSRGKLVOKLNWAMASDFNLFPVAIFQSSMTKVTKIGGQLKRIHQQLLF  
IMAVFIHNFKIPYNPQSQGVVTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSE  
EPIKIQNFRVYYRLTFGWCFKLQVPLRFMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVIPHY  
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGAGGAAAG  
CTGGTGGGGAAGCTGAACTGGGOCATGGCCAGCGATTTCAACTGCCCCCGTGGCCATCTTC  
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA  
GCTGCTGTTCATCATGGCCGTGTTTCATCCACAACTTCAAGATCCCCCTACAACCCCCAGAGCCA  
GGGGGTGGTGACCAACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCCGTGCACG  
GGGTGCAGATGGCCGTGTTTCATCCACAACTTCAAGGGCGCCGCGGTGTTTCATCCACAACTTCA  
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG  
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCTGAGGCCCATGACCTACAAGATGACC  
AACAAACCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG  
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG  
ACCCTG

FIGURE 18B

# HIV-TC

MGMQVQIQSLFLLLLWVPGRGYWQATWIFBWKAFQSSMTKKVYLAWVFAHKNAACFKVSFE  
 PIKHPVHAGPIANLTFOWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK  
 NQMVHQAI SPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGA AAVTVLDVGDAY  
 NAAARYLKDQQLNLTNFPISPINMTNNPPIPVNAFYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ  
 QVVKALLQLTVWGIGAAILKEPVHGVNAAAFPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI  
 YQEPFKNLKAAAVLAHAMSQVNLVGFPTVNI GAAAEBVNIVTDSQYKAAAPIHYCAPAKAVTYQY  
 MDDLYKAAAQMAVFIHNFKNATYQIYQEPFKFYNEWTLLEKAKIQNFRVYYRKAFVVRPQVPL  
 GAAAIWGC SGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTILNAAM  
 ASDFNLPVKSLNATDIAVNVTVYYGVFVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL  
 RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGA  
 GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG  
 AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGCTCTTGAA  
 CCCATTAAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTGCGGTGGTGCTTCAAA  
 CTAACAAATGATCGGCGGCGATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATTCT  
 TATAAAGCCGCTGCGCGTATACTCCAGCAGCTACTATTCATCAACACCACTCTCTCTGCGCTT  
 CAGACGCTAAGAACCAATGGTACACCAAGCCATAAGCCCTAGAGGAGCCAAGCTCGTAGGG  
 AAATTAATTTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGGATACCTGGAAGCAGC  
 CCAGGTTCCGTTACGCCCAATGACCTATAAAGGCGCAGCAGCAATAACAGTTCTAGATGTAGG  
 AGACGCTTACAACGCTGCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT  
 CCCAATTAGCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC  
 TCCAGTATTCCGAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT  
 ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT  
 TGGTGCTGCAATTCTAAAAGAGCCAGTTTATGGGGTTAAAGCCGCGCCTTCCCAATCAGTCC  
 TATTGAGACTGTGAAAGTATGGAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCGAGTTA  
 CAATTAATAATAGGGGGCCAACTTAAGAAAATATAACAGGAACCTTTCAAGAATCTCAAAAGCC  
 GCTGCAAGTGTCTCGCCGAGGCTATGTACAGGTGAATTTGGTCCGACCAACACCCGTAAACATC  
 GGAGCCGCAGCCGAAGTGAACATAGTCAACCGACTCACAGTACAAAGCCGCTGCAATACCCAT  
 ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC  
 CGCGCAGATGGCAGTCTTTATCCACAACCTTAAAAACGCAGCTACTTATCAGATCTACCAGGA  
 ACCATTCAAACCGTACAATGAGTGGACCTTGGAACTAAAGGCCAAAAATTCAGAACTTCAGGG  
 TATATTATAGAAAAGCATTTCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG  
 GATGTTCTGGAAAAGTGAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG  
 GCAGCCTGTTGGTGGGCAGGTATAAAGCAAAGTTCTGGCAGCATGGACGCTTAAAGCAGC  
 CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCAACCTTCCC  
 CCTGTAAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAAAGTAAACAGTATATTATGGCGTG  
 CCAGTCTGGAAAAAAGCCGCGCGGCCATAATTGGGATACTGCAGCAGCTGAAAAAGAGCTAT  
 GCGAGTGACTTCAACCTGAATGCGGCCGCTACCCCTTGGCATCGTTAAGGTCAGTATTTTG  
 A

FIGURE 18C

### HCV.1

MGMQVQIQSLFLLLLWVPGSRGDLNMGYIFLVYLVAAYQATVILAGYGAGVRLVFP  
DLGVHMWNFISGIYLLPRRGPRLYLVTRHADVVLVGGVLAALLFLLADAFLLADARVWMNRL  
IAFACTCGSSDLYLSAFSLHSYGVAGALVAFKLPGCSFISFKTSERSQPRLIFCHSKKKFWAKHMW  
NFIPFYGKAIRMYVGGVEHRQLFTFSRRRLGVRATRKVGIYLLPNRAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCC  
GGATCCAGAGGACTGCTGTTCAACATCCTGGGGGGGTGGGTGGATCTGATGGGGTACATCCCC  
CTGGTGTACCTGGTGGCCTAQCAGGCCACCGTGATCCTGGCCGGGTACGGGGCCGGGGTGAG  
GCTGATCGTGTTCOCOGATCTGGGGGTGCACATGTGGAACCTTCATCAGCGGGATCTAOCCTGCT  
GCCCAGGAGAGGACCTAGACTGTACCTGGTGAAGACACGCTGATGTGGTGGTGGTGGGAG  
GAGTGTGGCTGGCTGTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCTGCTGCTGGCTGATGCTAG  
AGTGTGGATGAACAGACTGATCGCTTTCGCTTGTACATGTGGAAGCTCCGATCTGTATCTGAG  
CGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGAGCTCTGGTGGCTTTTAAGCTGCCTGGATG  
TAGCTTTAGCATCTTTAAGACCAAGCGAAAGAGCCAGCCTAGACTGATCTTTGTACAGCAA  
GAAGAAGTTTTGGGCTAAGCACATGTGGAATTTATCCCTTTCTATGGAAGGCTATCAGAAT  
GTATGTGGGAGGAGTGGAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAG  
TGAGAGCTACAAGAAAGGTGGGAATCTATCTGCTGCCCTAATAGATGAAAGCTTGGG\*

### HCV.2

MGMQVQIQSLFLLLLWVPGSRGDLNMGYIPLVAKFVAAWTLKAAALLFLLADALIFCHSKKKQLF  
TFSPRRYLVTRHADVYLLPRRGPRLLCTCGSSDLYHMWNFISGIFWAKHMWNFAKFVAAWTLKAA  
AILAGYGAGVYLVAAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAALLADA  
RVLPGCCSFISAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLVFPDLGVWMNRLIAFALSFS  
LHSYLLFNILGGWVVGIYLLPNR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCTCCTGGTGGCTAAGTTTGTGGCTGCT  
TGGACACTGAAGGCTGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGTACA  
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT  
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC  
ATGTGGAACCTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTATCCTGGCTGGA  
TATGGAGCTGGAGTGATCTGCTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG  
GCTTTCAAGATCCATTCTATGGAAGGCTATCAGAATGTATGTGGGAGGAGTGGAACACAG  
AGTGTGGTGGGAGGAGTGTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGCTGCCAGG  
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCCAGCCTAGAAGACTGGGAGTGAGAGC  
TACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT  
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT  
GGGAATCTATCTGCTGCCAACAGATGAAAGCTT

### HCV.3s1

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLADALIFCHSKKKYL  
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNF\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGATACCTCGTGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC  
TGGACACTGAAAGCTGCAGCTGCTGCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT  
CCAAGAAAAAGTATCTGGTCAACAGACATGCTGACGTGCTGGGGTTTGGGCGCTACATGAGC  
AAGTGCACTGTGGCAGCTCCGACCTGTATCATATGTGGAACCTTTATTTCTGGAATCTTTGGG  
CCAAGCACATGTGGAATTTCTGAAAGCTT

FIGURE 18D

**HCV\_3a2**

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLADARVLSAFSLHSYIL  
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIIYLLPNR\*

GAATTGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGTCTGCTGGGCGGGCGTCTGGCCGCTGCTAAGTTTGTGCTGCT  
TGGACACTGAAGGCAGCCGCTTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCGCCTGCTGGCATTCAAGGTGCGGATC  
TACCTCCTGCTAACCCTGAAAGCTT

**HCV\_3a2(-3)**

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAKFVAAWTLKAAAFLLADARVLSAFSLHSYIL  
AGYGAGVWMNRLIAFA\*

GAATTGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGTCTGCTGGGCGGGCGTCTGGCCGCTGCTAAGTTTGTGCTGCT  
TGGACACTGAAGGCAGCCGCTTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCTGAGGATCC

**HCV\_3a3**

MGMQVQIQSLFLLLLWVPGSRGDLMOYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV  
RMYVGGVEHRLIVFPDLGVVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPRRYLLPRRGPRL

GAATTGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGACCTGATGGGCTACATCCTCTCGTGGCCAAGTTTGTGGCAGCT  
TGGACCTGAAAGGCGCTGCCAGACTGGGAGTGCAGCGCTACACGGAAACTCCTGTTTAAACATC  
CTGGGAGGGTGGGTGCGGATGTACGTGCGAGGCGTCCAGCACAGAAAGGCTCATTGTCTTTCC  
AGATCTCGGCGTGGGCGTCCAGGCGCACTGCTGGCCTTCAAACCTGCCAGGGTGACGCTTCAG  
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT  
CTGCTGCCAGACGCGGACCCAGGCTGTGAAAGCTT

**HCV\_PC3**

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD  
LGVKFWAKHWMNFIGVAGALVAFKKQLFTFSPRR\*

GAATTGCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGTCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCTGTG  
GCTGCTGGACCCTGAAGGCTGCGCTCTGGCCGACGGGGGATGCAGCGGCGGAGCTTACAG  
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTCATCGG  
GGTGGCCGGAGCCCTGGTCTTTTAAAAGCAGCTCTTCACCTTCTCCCAAGACGGTGAGG  
TACC

**FIGURE 18E**

**HCV.PC4**

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPQCSFSIFN  
DLMGYIPLVKYLLPRRGPRNLTLGGFADLMGYRMYVGGVVEHR\*

GAATTCGCGGCCACCATGCGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAAGGCTGGGGGTGAGAGCCACCCGGAAGAAGGCCAAGTTCCGTGGC  
TGCTTGACCCCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCAGCCCAGGAACCTGCCTG  
GATGCTCTTTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCC  
CAGACGGGGCCCTCGCCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTA  
TGTGCGCGGAGTCGAACACAGATGAGGTACC

**HCV.243I(1P)**

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAALFLLADARVLSAFSLHSYILAGYGAGVWMNRL  
IAPAGAAARLGVRATRKKAAAKTSERSQPRNLPQCSFSIFNDLMGYIPLVKYLLPRRGPRNLTLGG  
FADLMGYRMYVGGVVEHRKLLFNILGGWVKAALADGGCSGGAYRLVFPDLGVKFWAKHMWN  
FIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLADALIFCHSKKKYLVRHADVLG  
FGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKAAAAKFVAAWTLKAAA

GAATTCGCGGCCACCATGCGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGCTCCAGAGGAGTCTGTGGGGCGGGCTCCTGGCAGCCGCTTTCTGCTCCTGGCA  
GACGCCAGGGTGCTGTCTGCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGGCGAGGC  
GTGTGGATGAATCGGCTGATCGCTTTGCGGGCGCTGCCGCAAGGCTGGGGGTGAGAGCCACC  
CGGAAGAAGGCTGCCGCTAAAACAAGGAGCGCTCCAGCCCAGGAACCTGCCTGGATGCTC  
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG  
GGCCTCGCTGAACACTCTCTGTGGATTTGCTGATCTGATGGGGTACAGGATGTATGTGCGC  
GGAGTCGAACACAGAAAACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT  
GGCCGACGGGGGATGCAGCGCGGAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAA  
ATTTTGGGCAAAGCACATGTGGAATTTTCATCGGGGTGGCGGAGCCCTGGTGGCTTTTAAAAA  
CCAGCTCTTCACTTCTCCCCAAGACGGAACGGATACCTCGTGGCTACCAGGCCACTGTGGC  
TGCAGCTCTGCTCTTCTGCTCCTGGCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT  
CTGGTCAACAGACATGCTGACGTGCTGGGGTTTGGGCGCTACATGAGCAAGTGCACTGTGGC  
AGCTCCGACCTGTATCACATGTGGAACCTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG  
AATTTTAAAGCCCGCAGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG  
ATCC

FIGURE 18F

**HCY4312(1P)**

MGMQVQIQSLFLLLLWVP GSRORLOVRATRKKAAAKTSEBSQPRNLPCCSFSIFNDLMGYIPLVK  
YLLPRRGPRINTLOGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGC8GGAYRLIVFP  
DLGVKFWAKHMWNFIQVAGALVAFKKQLFTSPRNGYLVAYQATVAAALLFLLADALIFCHS  
KKKYLVTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLAA  
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGCTOCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAAAC  
AAGCGAGCGCTCCAGGCCAGGAACCTGCGTGGATGCTCTTTCAGCATCTTTAATGACCTCAT  
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG  
TGGATTTGCTGATCTGATGGGTACAGGATGTATGTGCGGGAGTCCGAACACAGAAAACTGCT  
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCGCTCTGCGCGACGGGGGATGCAGCGGCG  
GAGCTTACAGGCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA  
ATTTTCATCGGGGTGGCGGAGCCCTGGTGGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCAA  
GACGGAACGGGATACCTCGTGGCTACCGGCACTGTGGCTGCAGCTCTGCTCTTCTGCTCC  
TGGCGGATGCACCTCATCTTCTGCCATTCCAAGAAAGTATCTGCTCACCAGACATGCTGACG  
TGCTGGGGTTTGGGCGCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT  
GGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG  
TCCTGGTGGGCGGCGCTCCTGGCAGCGCTTTCTGCTCCTGGCAGACGCCAGGGTGTGCTGTG  
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGGCGAGGCGTGTGGATGAATCGGCTGA  
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAAGCAGCTGCATGAG  
GATCC

**AOSIK**

MGMQVQIQSLFLLLLWVP GSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVKFLLSLGIH  
LYMDDVVLGVGLSRYVARLFLRLITLPTTIVVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGGCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAGGCCAAGTTCGTGGCTGCCTGGACCCCTG  
AAGGCTGCCGCTTTCTGCTAGCGATTTCTTTCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA  
TCCACCTGTATATGATGACGTGGTGGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGCCTGT  
TCTGCTGACCCAGAAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG  
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA

**HBV.1**

MGMQVQIQSLFLLLLWVP GSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVFLSLGIHL  
YMDVVLGVGLSRYVARLFLRLITLPTTIVVRRQAFTFSPTYKWLSLLVPFVIPSSWAFTP  
ARVTGGVFKVGNFTGLYLPDFFPSVTLWKAGILYKNVSIPTWTHKLVVDFSQFSRAICSVVRRAL  
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGGCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAGGCCAAGTTCGTGGCTGCCTGGACCCCTG  
AAGGCTGCCGCTTTCTGCTAGCGATTTCTTTCTAGCGTGTTCCTGCTGTCCCTGGGAATCC  
ACCTGTATATGATGACGTGGTGGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTC  
TGCTGACCAGAACTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT  
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAG  
CTCCTGGGCTTTACCCAGCCAGGGTGACCGGAGGAGTGTTAAGGTGGGAAACTTCACCCGG  
CCTGTATCTGCCAGCGATTTCTTTCTAGCGTGAACCTGTGGAAGGCCGGGATCCTGTACAA  
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGGACTTTTCCAGTTCAGCAGATCCG  
TATCTGCTCCTGGTGAGGAGAGCTGTGATGOCCTGTATGCCTGTATCTGA

**FIGURE 18G**

**HBV.2**  
MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFPFSVNFLLSLGIIH  
LYMDDVVLGVQLSRYVARLFLTRILTISTLPETTVVRRQAFTFSPTYKGAAAWL8LLVFPVNPPI  
SSWAFKTPARVTGGVFKVGNFTGLYNLPSDFPFSVKTLWKAGILYKNVSIPTWTHKGAALVVDPSQ  
PSRNSAICSVVRRALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAAGTTGCTGGCTGCCTGGACCTG  
AAGGCTGCCGCTTTTCTGCTAGCGATTTCTTTCTAGCGTGAACCTCCTGCTGTCCCTGGGAA  
TCCACCTGTATATGGATGACGTGGTGTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT  
TCTGCTGACCAAGATCCTGAACATCTCCACCTGCCAGAGACCACCTGGGTGAGGAGGCAGG  
CCTTCAOCTTTAGOCCTACCTATAAGGGAGCCCTGCTGGCTGAGCCTGCTGGTGGCCTTTGT  
GAATATOCCTATCCTAGCTCCTGGCTTTCAAGACCCAGCCAGGGTGACCGGAGGAGTGT  
TAAGGTGGGAACTTCAACCGGCTGTATAACCTGCCAGCGATTTCTTTCTAGCGTGAAGAC  
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCTTGGACCCACAAGGGAGCCG  
CTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATTCCGCTATCTGCTCCGTGGTGAGGAGAG  
CTCTGATGCCACTGTATGCCTGTATCTGA

**PFCTL.1**  
MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAQTNFKSLRLNLPSENERGYKAAALLACAGLAY  
KKAATAKFVAAWTLKAAAKAFMKAVCBEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA  
TSVLKAGVSENIFLNAAAYFILVNLLKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAATCCTGAGCGTGTCTCTTTCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC  
CTCCTGAGGAACCTCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC  
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTGCTGGCCGCTTGGACACTGAAGGC  
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCTGTTT  
GTGGAGGCCCTCTTTAAGCTACTCCTTACGCAGGGGAACCAGCCCCCTTCAAGGCCGCTGCA  
AAATATAAGCTGGCAACAGCGTGTGAAAGCTGGCGTGTCCGAGAATATTTTCTGAAAAAC  
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAAGGCCGGACTCCTGGGGGTGGTCTCT  
ACAGTGTGA

**PFCTL.2**  
MQVQIQSLFLLLLWVPGSRGFVEALFQBYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA  
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDBENIGIYKLPYGRNLKAAAVLLGGV  
GLVLNFIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGATTGCTGGAGGCCCTGTTTCAGGAATACAAAGCCGCTGCAAAGTATCTCGTCATCGTGTT  
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTACTTCATTCTGGTCAACC  
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAAAGCCGCGAGCTAAGTTTGTGGCCG  
ATGGACCTGAAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTTCAAACTTCCAA  
GACGAGGAAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC  
AGTCTGCTCGCGGAGTGGGGCTGGTGTCAATTTTCTGATCTTCTTGATCTGTTCTCTGGT  
AAGGCCGCTCCTGGCCGGCCTGCTCGGAGTGTGTGA

FIGURE 18H

**PCTL3**

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD  
NEIKAHVLSHNSYBKNNYQKQENWYSLKKILSVFFLANAAAFKSLFHIFKAAAALYISFYFIKAKF  
VAAWTLKAAAKAAAYYIPHQSSLKAAAGLIMVLSFL

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAAGTGTCTGATCTTCTTTGACCTGTTCTGAAACGCCGCTGCACCCAGCGATGGCAAGTGC  
AATCTCTACAAGGCGCTGCAGTGACCTGTGGAACCGGATTTCAGGTTCAGGAAAATCTTTTAC  
ATCTTGCAGCGCGATAACGAGATCAAGGCCCATGTGCTGTCCACAAATCTTATGAAAAAAAC  
TACTATGGAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTGGCC  
AAGCGCGCTGCAAGGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA  
GCTTCTATTTTATTAAAGCCAAATTTGTGGCGCTTGGACACTGAAGGCCGCTGCAAAAGCCG  
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGTCTCT  
CTTCTCTGTGA

**PCTL/HILN**

MQVQIQSLFLLLLWVPGSRGSSVFNVNSSIGLIMVLSFLGPGPLYISFYFILVNLLIFHNGKIKN  
SEGP GPGPDSIQDSLKESRKLSGPGPGVLAGLLGVVSTVLLGGVGLVLPGLPSENERGYYPHQ  
SSLGPGPGQTNFKSLRLNLGVSENIPLKGP GPGQDBENIGIYGP GPGKYLIVFLIFFDLFLVGP  
GPKFKSLFHIFDGDNEIGP GPGKSKYKLATSVLAGLLGPGPLPYGKTNLGP GPGGRHNWVNHAVPL  
AMKLIGP GPGMRKLAILSVSSFLFVEALFQEYGP GPGVTCGNGIQVRGPGPMNYYGKQENWYSL  
KKGP GPGPSDGKCNLYADSAWENVKNVIGPFMKAVCBEVGP GPGKILSVFFLALFFIIFNKGP GPG  
HVLSHNSYBKGP GPGPKYKIAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAAGTAGTGTGTTCAATGTTGTGAACCTCATCAATTGGTCTGATCATGGTGTGAGCTTTCTCG  
GGCCAGGGCCAGGATTATATTTCTTTCTACTTCATCCTTGTCAACCTGTTAATATTCCACAT  
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT  
CTCTAAAAGAATCGAGGAAGCTCTCCGQACCAGGCCCTGGTGTACTCGCCGGGTTGTCTGGGA  
GTAGTTAGCACAGTGCTGTAGGAGGCGTCCGGCCTCGTCTTAGGACCTGGACCAAGTCTGCG  
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCAGGCCCGGACA  
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC  
CGGTCCCGGCTTTTCAGGACGAGGAGAATATAGGTATTTACGGTCCAGGACCTGGAAAATACT  
AGTGATCGTATTCTTAATTTTTTTGACCTATTTCTGGTGGGCCAGGTCCCGGAAAGTTTATT  
AAATCACTCTTCCACATTTTTGACCGAGATAACGAGATAGGACCCGGTCCCGGGAATCAAA  
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCAGGGCTCCCTATGG  
AAAGACAAATCTTGGCCCCGGTCCAGGACGGCACTGGGTGAATCATGCGGTTCCATTGG  
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT  
TTCTGTTCTAGAGGCACTGTTTCAAGAATATGGCCAGGACCTGGCGTCACATGTGGGAATG  
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACTATTACGGTAAACAGGAAAATTGGTAC  
TCCCTGAAAAAGGGTCCAGGCCCGGCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA  
GCATGGGAGAACGTAAAAAATGTAATAGGCCATTTCATGAAGGCAGTTTGTGTGGAAGTCGG  
ACCAGGCCAGGAAAAATACTTTCTGCTTCTTCTAGCTCTCTTCTTCATCATCTTCAACAAG  
GGACCAGGGCCAGGTACGTGTTATCCATAACTCTTATGAAAAAGGCCAGGACCTGGGAA  
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCCTGCGCAGGCTTGGCTTA  
CAAATTCGTTGTACCAGGAGCTGCAACACCTATGCAGGAGAACCTGCCCCATTTTGAAGATC  
TGC

**FIGURE 18I**



PE3

MGMQVQIQSLFLLLLWVPGSRGFMKAVCVBNVTCNGIQVRKGLIMVLSFLNAALFHIFDODN  
 EIKAAALLACAGLAYKKSFLFVBALFNAAPSDOKONLYKAAQTNFKSLRLNLPSENERGYKAAGVS  
 BNIFLKNAAYFILVNLLIKAAAILSVSBFLFVNTPYAGEFAPFKAAAKYKLATSVLKAAVFLIFFDL  
 FLNYYIPHQSSLKAAAGLLGNVSTVGAVLLGGVGLVNLACAGLAYKKAKFIKSLFHIFKAAFYFIL  
 VNLLKAFLIFFDLFLVKALFFIIFNKNYGKQENWYSLKFVBALFQBYNAAAKFVAAWTLKAAAK  
 ILSVFFLANAVLAGLLGNVNFQDBENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA  
 HVLSHNSYBKNAAAKYLVTFLI

GCGGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC  
 GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAAACATGCGGTAACGGAAT  
 TCAGGTGAGAAAAGGACTCATCATGGTACTCAGCTTTCTGAAOCGACGCCCTGTTCCACATCTT  
 TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCTGTGCGGACTAGCCTATAAAAAGA  
 GTTCTCTTTTCTGTTGAAGCACTATTTAAGGCAGCACCCAGTGACGGTAAATGCAACCTATATA  
 AAGCAGCTCAGACTAATTTCAAAGCCTGTTAAGAAATCTGCCCTCAGAGAATGAAAGGGGT  
 TACAAAGCCGCGCGGTGTCCGAGAATATTTCTGAGAAGACGCCGCTGCTTATTTTATACTC  
 GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCACTGTCCAGCTTTCTGTTTGTAAACACAC  
 CATATGCGGGCGAGCCGCTCTTTCAAAGGCTGCAGCAAAATACAAGCTTGCCACATCAGTAT  
 TGAAAGCAGCTGTGTTTGTATTTCTTTGATCTTTTAAACTACTACATACCTCATCAGTCT  
 AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCGCTCTTACTTGGAGGA  
 GTTGGCCTCGTGTGAAOCTCGCGTGCAGGTCTGGCCTACAAAAAGCGAAATTCATCAAG  
 TCTCTGTTCCACATTTTAAAGCCGCACTTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCT  
 GATCTTCTCGATCTATTCTGTAAAGGCTATTCTTCATTATCTTTAAACAAAAATTATTAC  
 GGAAGCAAGAAAAATTGGTACTCAAGTTTGTAGAAGCTCTGTTCCAGGAATACAACGCC  
 GCTGCTAAATTCGTTGCAGCTTGGACCGTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTC  
 TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG  
 GCATCTACAAAGCCGCAGCACTGTACATTTCACTTCTACTTCAAGGCCCTTCATACTGGTCAA  
 CCTTCTGATATTTCAATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCACGT  
 GTTGAGCCACAACCTCTACGAGAAGAAGCGCCGCGGAAATATCTCGTCAATTGTCTTCTGAT  
 TTGA

TE1

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMMIGTAAAVVKALVLLMLPVGA  
 GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRPLVLPVAVNAAAKFVAAWT  
 LKAAAKAAARLMIGTAAAGFVVALIPLVNAMTYAAPLFVGAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGAGGAAGG  
 ATGAGCAGAGTGACACATTCAGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTGCTGAAC  
 CTGATGATCGGCACCGCTGCAGCCGCTCGTGAAGGCTCTGCTGCTCATGCTCCTGTGGGA  
 GCAGGGCTGATGACAGCCGTGTACCTGGTGGCGCTGCAGCCATGGCCTCCTGCGGCTGCCA  
 GTGAAGCGCATGTTTGTGCAAACTGGGAGTCAACTCCTCTATTTCGGGGGCATTGCGGTG  
 GGAAGGCTGCCCTCGTGTGCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG  
 ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT  
 CGTGGTCCGCTGATTCCTGTTGAAGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC  
 CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA

FIGURE 18J

**BCL A2 #20**

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLQLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL  
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA  
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAATT  
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA  
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCCTGGCTTTTGTCAATGCC  
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCTACCTCCAGCTGGTCTTCGGCATCGAG  
GTCAAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCTCAAGGCTGCAGCAAAGGCTGCCGCC  
GTCTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGACTAGGGTCAATGCT  
GCCGCCCAACAGTGGGAATCATGATTGGGGTGAATGCCAAACTGTGCCAGTGCAACTGTG  
GGTGTGA

**BCL A2 #88**

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAACFVAAWTLKAAAKVAEIVHFLNAYLSGANL  
NVGAAYLQLVFGIEVNIMIGHLVGVNRLQLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV  
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAGTC  
GTGCTGGGAGTCGTCTTCGGCATTAAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCTG  
AAGGCCGAGCTAAAGTGGCAGAGATCGTGCACCTTTCTGAACGCCTACCTGAGCGGAGCAAA  
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTITGGAATTGAAGTGAACATCATGATTGG  
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAAACTGAGCTGGTCAACGCTAAAGTGTTCG  
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCGTCCAACTCTGGGTCAATGCCGAGCCG  
CTACAGTGGGGATCATGATCGGCGTGAACCTCCATGCCTCCACCAGGGAACAGAGTGTGA

**BCL A2 #63**

MQVQIQSLFLLLLWVPGSRGKLCVPQLWVNAAAATVGIMIGVNIMIGHLVGVNRLQLQETELVNA  
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA  
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGAAAAG  
CTCTGCCCGGTGCAACTGTGGGTCAACGCCCGCGCGCAACCGTCGGCATTATGATCGGGGTG  
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA  
TGCCAAGGTGGCTGAAATTGTCCATTTCCTGAATGCCAAAGTGTTCGGCTCTCTCGCTTTCTGTG  
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG  
ATTGAGGTGAATGCCGAGCTAAATTGTGCTGCTGCCTGGACCTGAAGGCAGCAGCCAAGGCT  
GCCGAGTGGTGTGGGAGTGGTGTITGGAATCAATTCCATGCCTCCACCAGGCACTAGAGTG  
TGAGGATCC

**FIGURE 18K**

**Protein 1.**

LTFFWLDRSVKAAAVLVHPQWVLTVKAAALLQBRGVAYIKAALLLSIALSVNPLVCNGVLQGVK  
AAIMYSAHDTTVKAAAF LTPKKLQCVNAMMNDQLMFLNAGLPSIFVHPVKAAALGTTTCYVGAAL  
LLWQPIFVNFLRPRSLQCVKAF LTLSTWIGVNALLYSLVHNLOAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTO  
ACATTTTTTTGGCTGGATAGATCGGTTAAGGCTGCAGCCGTGCTTGTTTCATCCCAAGTGGGTCT  
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTCCGATACATCAAAGCTGCTCTC  
CTCTTGAGTATTGCGCTAAGTGTAACCCGCTAGTTTGTAAATGGGGTGTTACAAGGTGTGAAA  
GCGGCGATTATGTACAGTGCCCAAGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA  
AAACTCCAATGCGTGAAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT  
TCTATACCGGTTTCATCCAGTCAAGGCCCGCGGCATTGGGTACGACGTGTTATGTTGGAGCAGCG  
ATACTTCTTTGGCAGCCCATACAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG  
CATTCTTACACTCTCACTAAGTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA  
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTCGTGGCGGCCTGGAC  
TCTAAAGGCCGCGACGA

**HIV-1043**

MEKVYLA WVP AHK GIGGGP GPGQK QITK IONFR VY YRGP GPW EFNTP PLVKL WYQ GP GPYR  
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGP GPGGEIYKRWILGLNKIVRMYGPGPGQQM  
VHQAI SPTLNGP GPGIKQFINMWQEVGKAMYGP GPGWAGIKQBFIPYNPQGP GPGKTA VQMA  
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNVTD SQYALGHP GPGHSNWRAMASDFNLFP  
GPGPGAETFYVDGAANRETKGP GPGGA VVIQD NSDIK VVP GPGPGFRKYTAFTIP SINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCCAAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGA ACTTCCGGGTATACTACCGGGGACCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCAACCCTTAGTAAAGCTCTGGTAACAGGGCCCCGGTCCCGGAT  
ACCGTAAATCCTGAGGCAAAGAAAAGATAGATCGCCTCATTGATGGCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAAGTCGACGGGGCCGGGCCCGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCCTGAATGGACCGGGGCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGGGAATCCCTTACAATCCCCAGGGTCTGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTCAATTCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC  
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCAGGGCCGGGGCAAGT  
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCCGACCAAGGGCATTCCAA  
TTGGGCGGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAACTTT  
CTATGTGGACGGCGCTGCAAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA  
TTCAGGACAACTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCGGGTTCAGAAA GTATACCG  
CCTTCACTATTCCGTCCATCAACAATGAGTGA

**FIGURE 18L**

**HIV-1043 PADRE**

MEKVYLA WVP AHK GIGGGP GPGQK QITKI QNFRVYYR GP GPGWBFV NTPPLVKLWYQGPGPGYR  
KILRQRKIDRLIDGPGGQHLLQLTVWGKQLQGPGPGGEYKRWIILQNKIVRMYPGPGQGGQM  
VHQAI SPRTLNGP GP OIKQFINMWQEVOKAMYGP GPGWAGIKQBF GIPYNPQPGPGKTAVQMA  
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGBEVNIVTDSQYALGHPGPGHSNWRAMASDFNLPP  
GPGPGAEIFYVDGAANRETKGPGPGGAVVIQD NSDIKVVP GPGPGFRKYTAFTIP SINNBGPGPGA  
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCCACAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGAOCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCAACCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCGGAT  
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGGAATTAACAGCTGCAGGGGGCCGGGCCCGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAAGTTGGTAAGGCTATGTACGGTCCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGGAAATCCCTTACAATCCCCAGGGTCTGGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTCAATTCATAATTTAAGCGGGGCCCTGGAOCTGGCAGC  
CCAGCTATATTTCAAAGTTCGATGACGAAAATCTTGGAGCCCGGCCAGGGCCGGGGCGAAGT  
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAAGGGCCCGGACCAGGGCATTCCAA  
TTGGCGGGCCATGGCGTCTGACTTTAATCTAOCCTCCTGGGCCAGGCCCTGGCGGGGAAACTTT  
CTATGTGGACGGCGCTGCAAAACAGGGAGACTAAGGGGACCCGGACCCGGCGGGGCTGTAGTCA  
TTCAGGACAACCTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCGGGTTTCAGAAAGTATAACCG  
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGGCCAGGTGCCAAGTTCTGTGGCTGCCCT  
GGACCCTGAAGGCTGCCGCTTGA

**HIV 75mer**

EKVYLA WVP AHK GIGGGP GPGQGMVHQAI SPRTLNGP GPGSPAIFQSSMTKILEP GPGPGFRKYTA  
FTIP SINNB

GAGAAGGTGTACCTGGCCTGGGTGCCCTGCCACAAGGGAATCGGAGGACCTGGCCCTGGACA  
GGGACAGATGGTGCAACAGGCCATCAGCCCTAGGACCTGAACGGACCTGGACCTGGAAGCC  
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTGAGGA  
AGTACACCGCCTTACCATCCCCAGCATCAACAACGAGTGA

**FIGURE 18M**

**PHIL**

**MQVQIQSLFLLLLWVPGSRORHNWYNHAVPLAMKLIQPGPKCNLYADSAWENVKNQPGPGKS  
KYKLATSVLAGLLGPGPGQTNFKSLRLNLGVSEGPFGSSVFNVNSSIOLIMGPGPOVKNVIGPF  
MKAVCVEGPGPGMNYGKQENWYSLKKGPFGGLAYKFVVPDAATPYGPGPGPDSIQDSLKESR  
KLNQPGPOLLIFHINGKIKNSEGPFGAGLLGNVSTVLLGGVQPGPGKYKIAGGIAGGLALLGPGP  
GMRKLAILSVSSFLFV**

**ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCTGTGGGTGCCCGGATCCAGA  
GGAAGGCACAACCTGGGTGAATCATGCTGTGCCCTGGCTATGAAGCTGATCGGCCCTGGACC  
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG  
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCTGTCTCGGACCAGGCCCGGAC  
AGACAAATTTCAAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGGCCAGGATCT  
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA  
AATGTCATTGGCCCATTCATGAAGGCCGTGTGTGTCGAAGGACCCGGGCTGGCATGAACTAC  
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGOCAGGCGGACTGGCTTA  
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCTGGGCCAGGCCCGGATTCCATCCA  
GGACTCTCTCAAAAGAGAGCCGGAAACTGAACGGAACCGGGCCTGGACTGCTCATTTTCCACAT  
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGGAAGTGTGGGGAACG  
TGTCCACCGTCTGCTCGGGGAGTGGGGCCCGGCCCTGGGAAGTACAAGATCGCTGGAGGG  
ATCGCAGGCGGACTGGCCCTGCTGGGCCAGGACCGGGATGGGCAAACCTGGCTATTCTCTCT  
GTCTCCAGCTTTCTGTTTGTGTGA**

**FIGURE 18N**

Protein	Sequence	Restriction
HIV gag 386	VLARMSQV	HLA-A2
HIV gag 271	MTNNFPIPV	HLA-A2
HIV pol 774	MASDFNLFPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFFISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIIV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIRILQQL	HLA-A2
HIV vpr 62	RILQQLLI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIONFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVFVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAI SPR	HLA-A3
HIV gag 545	YFLASLRSLF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEP	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VITYQYMDPLY	HLA-A1
HIV pol 295	VTVL DVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTIPVFAI	HLA-A24
HIV pol 530	TYQIQEFP	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGC SGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A

Protein	Sequence	Restriction
HIV env 65	VWKEATITLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMV	HLA-DR
HIV pol 596	WBFVNTPLVLKLYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGIKQLQ	HLA-DR
HIV gag 171	QGQMVHQAI SPRTLN	HLA-DR
HIV pol 835	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIP SINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLFP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpr 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEFGITPNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGI	HLA-DR3
HIV pol 619	AEIFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDNSDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 182	DLMGYPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPR	HLA-A2
HCV NS1/E2 726	LLFLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSHRSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSRR	HLA-A3
HCV NS1/E2 632	RMVVGGEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDP9HITA	HLA-A1

FIGURE 19B

Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGC8GGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCBEV	HLA-A2
P. falciparum EXP1-83	GLLGTVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFHFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIEH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQBY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQBNWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLV	HLA-DR
P. falciparum CSP-53	MNYYGKQBNWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C



Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGFFMKAVCVB	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIKNSE	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRN LGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILT	HLA-A2
HBV env 335	WLSLLVPPV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTIVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDPSQESR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSPDFFPSV	HLA-B7
HBV env 313	IPISSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLFPV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPV	HLA-A2
TB	RLMIGTAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLFLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGIMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D

Protein	Sequence	Restriction
Her2/neu 665	VVLGVVVGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLFSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.8.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGITCYV	HLA-A2
PSA.161	FLTFKKLQCV	HLA-A2
HuK2.4.L2	LLSLIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E

Figure 20A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN <sup>1</sup>
924.07	core 18	FLPSDFPFSV	45	A2	3.5	5
777.03	env 183	FLLTRILT	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	GLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLOV	90	A2/A1	6.4	5
927.11	pol 562	FLSLGIHL	95	A2	7.8	3
927.15	pol 642	ALMPLYACI	95	A2	12.9	4
1083.01	core 141	STLPETIVVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1069.15	pol 150	TLWKAGILYK	100	A3/A11	2.1 / 33	2
1069.20	pol 388	LVVDFSQFSR	100	A3/A11	6875 / 17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174 / 117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189 / 29	3
1142.05	pol 629	KVGNFTGLY	95	A3/A1	58 / 365	2
1090.10	pol 665	QAFIFSPTYK	95	A3/A11	249 / 8	3
988.05	core 19	LPSPDFPFSV	45	B7	3026.8	4
1145.04	env 313	IPFSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPILL	100	B7	56.6	4
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRBTVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	BYLVSPGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3

<sup>1</sup>XRN = Cross binding, number of HLA types in the supertype panel of 5 for which significant binding as detected



Figure 20C

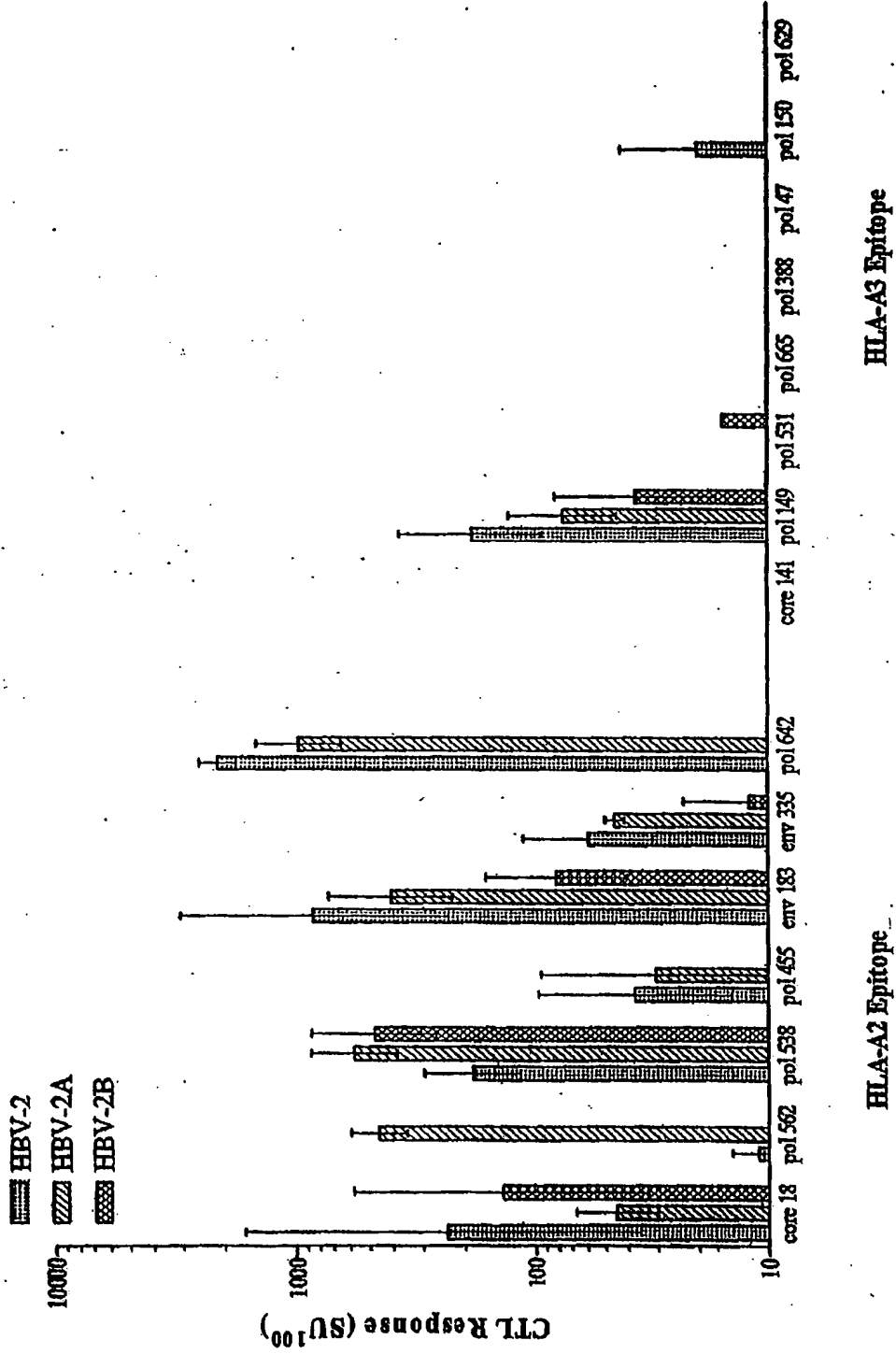


Figure 20D

HBV-2

5 MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAANTLKAAAFLP8DFFPSVNFLSLGIHLYMDDVVL  
GVGLSRYVARLFLL/TRLITISTLPETTVVRRQAF78PTYKGAAAWLSLLVPFVNIPIPSWAFKTPARVTGG  
VFKVGNFTGLYNLP8DFFPSVKTLWKAGILYKNVSIPTWTHKGAALVVD8QFSRNSAICSVVRRALMPLYACI

10 ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC  
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCCTGAAGGCTGCCGCTTCTCTGCC  
TAGCGATTTCTTTCTAGCGTGAACCTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG  
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCTGCTGACCCAGAATCCTGACCATCTCCACCCCTGCCAG  
15 AGACCACCGTGGTGAGGAGGCAGGCCCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCCTGGCTGAGCCT  
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGACCCGAGGA  
GTGTTTAAAGGTGGGAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTCTAGCGTGAAGACCCCTGT  
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT  
15 TTCCAGTTTACGAGAAATCCGCTATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCCTGTATC  
TGA

Figure 20E

HBV-2A

20 MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAANTLKAAAFLP8DFFPSVNFLSLGIHLYMDDVVL  
GVGLSRYVARLFLL/TRLITISTLPETTVVRRQAF78PTYKGAAAWLSLLVPFVNIPIPSWAFKTPARVTGG  
VFKVGNFTGLYNLP8DFFPSVKTLWKAGILYKNVSIPTWTHKGAALVVD8QFSRNSAICSVVRRKAWMMWYWG  
PSLYKKYTSFPWLLNAHPAAMPHLLKAAADLLDTASALYNAAARFSWLSLLVPFNAASWPKFVAVPNLKLTFGR  
ETVLEYKALSLDVSAAFYGAAYLV8FGVWGAALMPLYACI

25 ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC  
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCCTGAAGGCTGCCGCTTCTCTGCC  
TAGCGATTTCTTTCTAGCGTGAACCTCCTGCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG  
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCTGCTGACCCAGAATCCTGACCATCTCCACCCCTGCCAG  
AGACCACCGTGGTGAGGAGGCAGGCCCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCCTGGCTGAGCCT  
GCTGGTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGACCCGAGGA  
30 GTGTTTAAAGGTGGGAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTCTAGCGTGAAGACCCCTGT  
GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT  
TTCCAGTTTACGAGAAATAGCGCCATCTGTTCCGGTCTGAGAAGGAAAGCCTGGATGATGTGGTACTGGGQT  
CCTAGTCTGTATAAGAAGTACACCTCATTCCTATGGCTCTTGAATGCCCATCCCGCTGCAATGCCACACCTGC  
TTAAAGCTGCGGCGGATCTGCTGGACACAGCCTCAGCTTTATATAATGCTGCAGCAAGATTCTCCTGGTGTGC  
TCTCTTAGTGCCCTTCAACGCAGCTTCTGGCCAAAATTTGCCGTTCCGAACCTGAAGCTCACTTTTGAAGA  
35 GAGACAGTACTTGAATACAAAGCACTAAGCCTTGACGTGTACAGCAGCCTTCTACGGAGCAGCAGAATATCTAG  
TATCTTTTGGGGTCTGGGGGCGCAGCCCTCATGCCTCTATACGCCTGCATTTGA

Figure 20F

HBV-2B

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAANTLKAAAFLPDFFPSVNFLLSLGIHLYMDVVVL  
GVGLSRYVARLFLL/TRLTISTLPETTVERROAFTFSPTYKGAAWLSLLVPPVNIPIPSWAFKTPARVTGG  
5 VFKVGNFTGLYNLPDFFPSVKTLWKAGILYKNVSIPTWHKGAALVVDPSQPSRNSAICSVRRKBYLVSPGV  
WGLSLDVSAAFYNAAKYTSFPWLLNAHPAAMPHELLKAAADLLDTASALYNSWPKFAVPNLKLTFGRETVLEY  
KAAWMMWYWGPSLYKAAARFSLWLSLLVPPGAAALMPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGACACACCC  
TGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCTGTGGCTGCCCTGGACCTGAAGGCTGCCGCTTTCTGTCC  
10 TAGCGATTTCTTTCTAGCGTGAACCTTCTGTCTGTCCCTGGGAATCCACCTGTATATGGATGACGTGGTGCTG  
GGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCCTGTGACCAGAATCCTGACCATCTCCACCCGTGCCAG  
AGACCACCGTGGTGAGGAGGCAGGCCCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCCTGGCTGAGCCT  
GCTGCTGCCCTTTGTGAATATCCCTATCCCTAGCTCCTGGGCTTTCAAGACCCAGCCAGGGTGACCGGAGGA  
GTGTTTAAGGTGGGAAACTTCACCGGCCCTGTATAACCTGCCAGCGATTCTTTCTAGCGTGAAGACCCGTGT  
15 GGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCGCTCTGGTGGTGGACTT  
TTCCCAAGTTCAACAGAAATTCAGCAATTTGTTCCGTTGGTGAGAAGAAGGAATATCTTGTTTTCATTTGGCGTC  
TGGGGGCTGTCACTGATGTAAGTGCGGCATTTTACAATGCCCGCGCAAAATATACAAGCTTCCCATGGCTCC  
TAAACGCACACCCAGCTGCAATGCCGCATCTACTGAAAGCAGCCGCTGACCTCTTAGACACTGCCCTCCGCTCT  
GTACAACTCTTGGCCCAAGTTTGGCGTGCCCTAATCTCAAGTTGACCTTCGGTAGAGAGACAGTCTTAGAATAC  
20 AAAGCGGCTGGATGATGTGGTACTGGGGACCCCTCTCTGTATAAAGCCGCTGCAAGGTTCTCCTGGCTTAGCC  
TTCTCGTACCATTCCGAGCAGCTGCCCTAATGCCCTTTGTACGCATGCATCTGA

Figure 21A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLP8DFFPSV	45	A2	3.5	5
777.03	env 183	FLLRILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
927.11	pol 562	FLSLGIHL	95	A2	7.8	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
1089.01	core 141	STLPETTVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1090.11	pol 531	SAICSVRR	95	A3/A11	2189 / 29	3
1090.10	pol 665	QAFIFSPTYK	95	A3/A11	249 / 8	3
1145.04	env 313	IPISSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPILL	100	B7	56.6	4
1147.05	pol 530	FPHCLARSYM	95	B7	58.5	5
1039.06	env 359	WMMWYWGPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTPGRETVLEY	75	A1	80.0	3
1090.07	pol 415	LSLDVSAIFY	95	A1	6.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.07	core 117	BYLVSRGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3



Figure 21B

HBV 21A

signal	Ⓟ PANCE		Core		Pol		Env		Pol		Core		Pol		Env		Pol		Core		Pol	
	Pol	392	Core	141	Pol	429	Env	149	Pol	183	Env	415	Pol	745	Env	332	Pol	354	Env	530	Pol	359

HBV 21B

signal	Pol	Core	Core	Pol	Env	Pol	Env	Pol	Env	Env	Env	Env	Pol	Pol	Core	Pol	Core	Env	Core	Pol	Pol
	538	117	419	149	18	530	332	392	665	531	183	313	359	354	562	137	429	141	335	415	745
	A2	A24	A1	A3	A2	B7	A24	A24	A3	A3	A2	B7	A1	B7	A2	A1	B7	A3	A2	A1	A24

Figure 21C

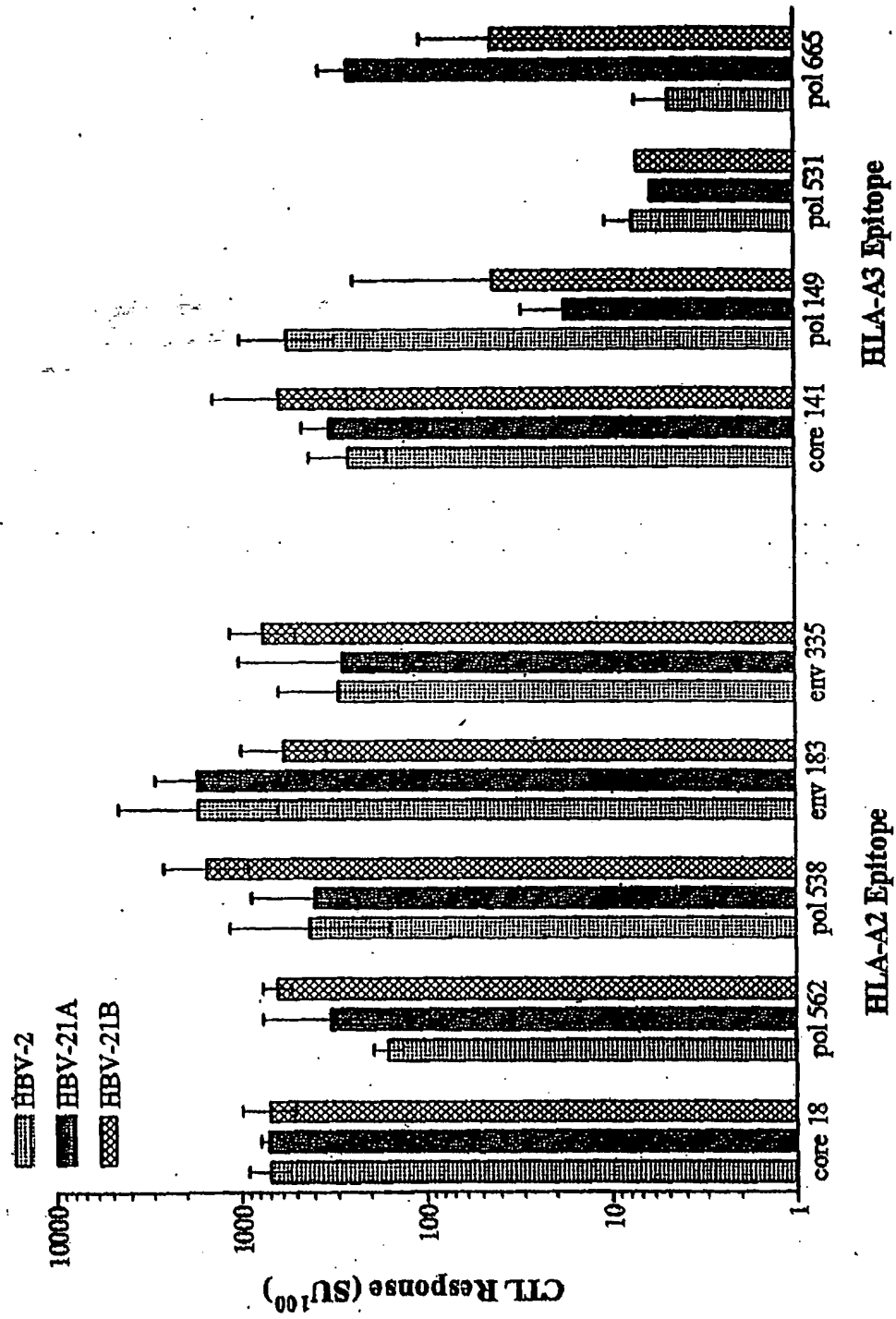


Figure 21D

HBV-21A

5 MGMQVQIQSLFLLLLLVPGSRGSPKFAVFNLKAAAACFVAAWTLKAAAKSTLPETTVVRRKHPAAMPHELLKA  
AAHTLWKAGILYKKAFL/TRLITIGALSLDVSAAFYNAAKYTSFPWLLNAAARFSLSLLVPFNAATPARVT  
GGVFKAAYLVSPGVWGAAAYMDDVVLGVNDLLDTASALYNAAAFPHCLAFSYMKAAMMMWYWGSPSLYKAAS  
AICSVVRRKNFLLSLGIHLNIPIPSSWAFKAAWLSLLVFPVNAFLPSDFPFSVKLTFGRETVLEYKQAFTFSP  
TYK

10 ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATCCTGGC  
CTAAATTCGCAGTGCCAAACCTTAAAGCCGCGCTGCTAAGTTCTGTAGCTGCTGGACACTAAAGGCCGCGC  
TAAGAGCACACTGCCAGAGACCACCGTGGTCCGCGGAAAGCATCCAGCCGCAATGCCCACTTGCTCAAAGCA  
GCCGCCACACTCTTTGGAAGGCTGGGATATTGTACAAGAAAGCCTTCCTTCTGACCAGGATATTAAGTATCG  
GAGCTCTGTCACTCGACGTTTCTGCTGCCTTCTACAACGCGCGGCAAAATACACTAGCTTTCCATGGCTACT  
CAACGCAGCCGCCAGATTTTCTTGGCTATCACTACTGGTGCCATTTAATGCAGCAACACCTGCTAGAGTGACT  
GGCGGCGTCTTTAAAGCAGCCGAGTACTTGGTGAGCTTTGGCGTCTGGGGTGCAGCGGCATATATGGATGATG  
15 TAGTGTTAGGGGTGAACGACCTCCTGGACACAGCCAGTGCGCTGTACAATGCAGCTGCATTCCCGCATTTGCC  
AGCCTTCAGTTATATGAAAGCAGCAGCCTGGATGATGTGGTACTGGGGACCGTCCCTTTATAAAGCAGCTTCA  
GCAATCTGTTCCGTTGTGAGGAGAAAAAATTTTTACTCTCCCTCGGTATTACCTGAACATTCCCATCCCTT  
CCTCATGGGCATTCAAAGCCGCTTGGCTGAGTCTACTCGTACCTTTTCGTTAATGCATTCTGCCCAGCGACTT  
20 TTTCCCTCGGTAAACATGACATTCCGACGCGAAACAGTCTTGAATATAAGCAGGCCTTCACGTTCTCACC  
ACCTATAAATGA

Figure 21E

HBV-21B

25 MGMQVQIQSLFLLLLLVPGSRGYMDDVVLGVNAAAEYLVSFGVWNDLLDTASALYGAHTLWKAGILYKKAFL  
PSDFPFSVKAFPHCLAFSYMKAARFSLSLLVPFNAASWPKFAVFNLKAAAQAFTFSPYKNAASAICSVVR  
RKAFLLTRILITINIPIPSSWAFKAAWMMWYWGSPSLYKAAATPARVTGGVFKAANFLLSLGIHLNLTFGRETVL  
EYKHPAAMPHELLKAASTLPETTVVRRKWLSSLVFPVNAAAAFVAAWTLKAAAKSLDVSAAFYNAAKYTSF  
PWLL

30 ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATACATGG  
ATGACGTTGTGTTAGGCGTTAATGCAGCCGAGAAATATCTCGTGTCAATTCGGCGTCTGGAAACGACCTGTTGGA  
CACTGCATCTGCTCTGTACGGTGCAGCCCATACCTGTGGAAAGCCGGAATCCTCTACAAAAGGCATTCTTA  
CCTAGCGACTTTTTCTTCACTGAAAGCCTTCCACATTGCCCTAGCATTCTCGTATATGAAAGCGGCTAGGT  
TCTCATGGCTTAGTCTTCTAGTACCTTTCAATGCCGCGCTCCTGGCCCAAATTGCGCGTACCAATCTAAAAGC  
GGCCGCGCAGGCTTTACATTCTCTCCGACTTATAAAAATGCAGCAGCCTCCGCTATTTGTAGCGTGGTGC  
CGAAAGGCCCTTCTGCTAACCAGGATTTTGACGATAAACATCCCCATCCCTTCTAGCTGGGCTTTCAAAGCAG  
35 CATGGATGATGTGGTACTGGGGTCCCAGCTTATACAAAGCTGCGGCAACCCAGCAAGAGTGACAGGGGGCGT  
GTTTAAGGCCGCCAACTTCTCTGAGTCTCGGAATACACCTGAACCTTAACCTTTGGGAGAGAGACAGTACTG  
GAGTATAAACACCCAGCAGCTATGCCGCACCTACTCAAAGCCGCTTCAACACTCCAGAAACAACCTGTAGTGA  
GGAGAAAAATGGCTCTCCCTGCTTGTCCCATTTGTCAACGCGCGCGCTAAGTTTGTGGCGGCTTGGACACT  
TAAGGCTGCAGCAAGTTGTCACTTGATGTTAGTGACGCTTCTATAACGCAGCTGCAAAATACACTTCTTT  
40 CCCTGGCTGCTGTGA

Figure 22A

ID#	Epitope	Sequence	Conservation	HLA restriction	Prototype Binding	XRN
924.07	core 18	FLPSDFPPSV	45	A2	3.5	5
777.03	env 183	FLTRIILTI	80	A2	9.8	4
1013.01	env 335	WLSLLVPFV	100	A2	5.4	4
1168.02	pol 455	QLSRYVARL	55	A2	55.9	3
1090.77	pol 538	YMDDVVLGV	90	A2/A1	6.4	5
927.11	pol 562	FLSLGIHL	95	A2	7.8	3
1083.01	core 141	STLPETTVVRR	95	A3/A11	735 / 4.5	4
1147.16	pol 149	HTLWKAGILYK	100	A3/A1	15.4 / 15.6	5
1069.20	pol 388	LVVDPSQFSR	100	A3/A11	6875 / 17	3
1069.16	pol 47	NVSIPWTHK	100	A3/A11	174 / 117	3
1090.11	pol 531	SAICSVVRR	95	A3/A11	2189 / 29	3
1090.10	pol 665	QAFITSPITYK	95	A3/A11	249 / 8	3
988.05	core 19	LPSPDFPPSV	45	B7	3026.8	4
1145.04	env 313	IPIPSSWAF	100	B7	42.3	4
1147.04	pol 354	TPARVTGGVF	90	B7	13.2	2
1147.02	pol 429	HPAAMPHLL	100	B7	56.6	4
1147.05	pol 530	FPHCLAFSYM	95	B7	58.5	5
1359.01	pol 640	YPALMPLYACI	95	B7	1393.4	3
1039.06	env 359	WMMWYWQPSLY	85	A1	16.3	3
1448.01	core 419	DLLDTASALY	75	A1	2.3	3
1373.88	core 137	LTFGRETVLEY	75	A1	80.0	3
1373.78	pol 166	ASFCGSPY	100	A1	247.0	3
1090.07	pol 415	LSLDVSAAFY	95	A1	6.0	3
1069.08	env 249	ILLCLIFLL	100	A1	192.0	1
20.0269	env 236	RWMCLRRFII	95	A24	11.0	3
20.0271	pol 392	SWPKFAVPNL	95	A24	2.1	2
1373.56	env 332	RFSWLSLLVPF	100	A24	12.0	2
1373.38	core 101	LWFHISCLTF	85	A24	6.7	3
1373.07	core 117	BYLVSEFGVW	90	A24	16.0	2
1069.23	pol 745	KYTSFPWLL	85	A24	1.0	3



Figure 22C

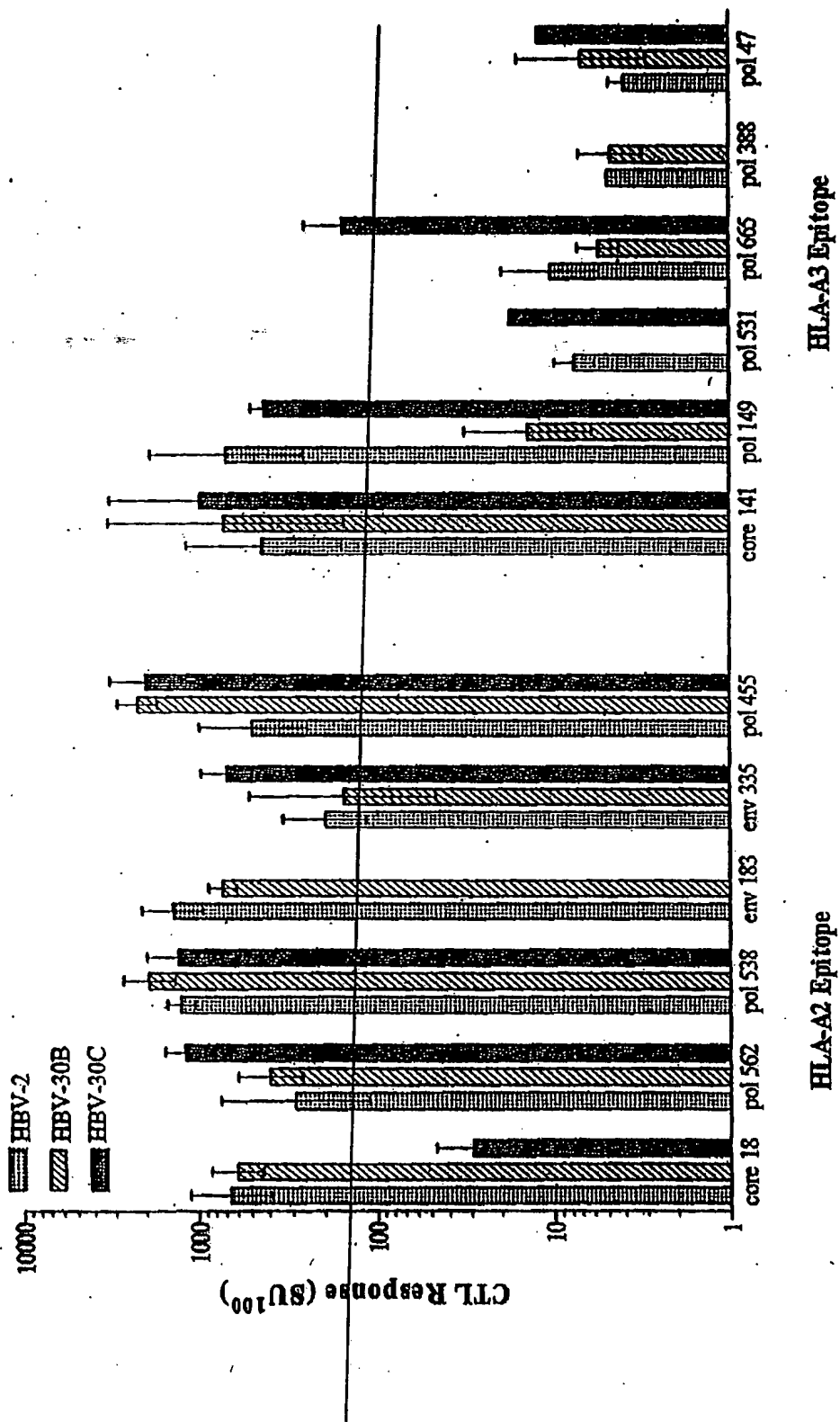


Figure 22D

HBV-30B

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5 QAFTFSPYKGAANVSIPTWTHKGAALFLLSLGIHLNIPISBWAFAAALWFHISCLTFKAAAILLLCLIFL  
LNAAAYPALMPLYACINAHPAAMPHELLKAAASFCGSPYKAAGLSRYVARLNKYTSFPWLLNFLPSDFFPSVKA  
FPHCLAFSYMKAHYLVSGVWNAALTFGRBTVLEYKAAALPSDFFPSVKAYMDDVVLGVNLVVD78QPSRNA  
ARWMCLRRFIINAARFSLVLPFNAAATFARVTGGVFAAHLVLPFVNSAICSVVRRKAKFVAAWTLKAA  
AKWMWYWGSPSLYKAASLPETTTVRRKLSLDVSAAPY  
10 ATGGGAATGCAGGTCCAGATACAGAGCTTGTTCCTCCTCCTGCTTTGGGTCCCGGATCAAGGGGTTTCCTCC  
TAACCGCATCCTGACAATTAACGCCGAGCCTCCTGGCCAAAATTTGCCGTGCCAAATCTCAAGGCAGCTGC  
ACACACACTTGGAAAGCAGGGATACTGTACAAGAAAGCCGATCTGCTAGACACAGCGTCTGCCGTTGTACAAC  
CAGGCTTTTACTTTCTCTCTACATATAAAGCGCAGCTGCAACCGTGAGTATCCCTTGGACGCACAAAGGAG  
CCGCTGCCAAGCTTCTTACTGTCCCTGGGCATCCATCTAAATATCCCTATTCCTTCATCTGGGCATTAAAGC  
15 AGCCGCCCTTATGGTTCCACATAAGTTGTCTGACCTTCAAAGCCGAGCAATCCTGCTCCTTTGCCCTCATTTTC  
TTACTAAACGCCGCTGCTATCCAGCTCTTATGCCATTGTACGCATGTATCAACGCCACCCCGCAGCAATGC  
CCCACCTCCTTAAAGCTGCCGCCAGTTTCTCGGCTTCTCCTTATAAAGCAGCAGGGCTGTCCAGATACGTAGC  
TAGGCTAAACAAGTATACCAAGCTTCCCTCGGTTACTTAATTTCTGCGCTCAGATTCTTTCCATCAGTTAAG  
GCCTTCCCTCATTGTCTGCGCTTTAGCTACATGAAGGCTGAATATTTGGTATCCTTCGGCGTGTGGAATGCCG  
20 CACTGACATTTGGAAGGGAGACAGTGTCTGAGTACAAAGCCGCCACTACCCCTCGGACTTCTTCCCATCGGT  
CAAAGCTTACATGGACGATGTAGTCTCGGCGTTAACTTAGTAGTGGACTTTTCTCAATTTTCCAGAAACGCA  
GCGGCCAGATGGATGTGCCCTTCGGCGTTTATAATAAAGCCGCTCGATTGAGCTGGCTATCAGCTCCTTAGTTC  
CATTTAATGACAGTACACCCGACGGGTGACAGGTGGAGTTTCAAGGCAGCGTGGCTTTCACTGCTTGTGCC  
ATTTGTGAACCTCAGCTATTTGCTCAGTAGTGAGAAGGAAGGCAAAATTCGTCGCTGCGTGGACTCTCAAAGCT  
25 GCCGCAAAGTGGATGATGTGGTATTGGGGACCGAGCTTGTACAAAGCGGCTCTACTCTGCCAGAACTACCG  
TAGTGAGAAGAAAAGTGGACCTGGACGTGACGCGCGCATTTACTGA

Figure 22E

HBV-30C

MGMQVQIQSLFLLLLWVPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSLVLPFNAAFPHCLAFSYMKA  
30 AALVVD78QPSRGAILLLCLIFLLNAAHTLWKAGILYKAWMMWYWGSPSLYKAYPALMPLYACIGAAWLSL  
LVPFVNFLLTRILTINIPISBWAFAAAYLVSGVWNLPSDFFPSVKFLPSDFFPSVKDLLDTASALYNSW  
PKFAVAVPNLKAAASAIKSVVRRKLSLDVSAAFYNAAKFVAANTLKAAAKAANVSIPTWTHKGAALSRVVARLN  
AAASTLPETTTVRRKHPAAMPHELLKAAARWMCLRRFIINAFSGSPYKAAYMDDVVLGVNALWFHISCLTFKA  
AATPARVTGGVFAAALTFGRBTVLEYKQAFTFSPYK  
35 ATGGGAATGCAGGTGCAAAATACAGTCTCTCTCTCTCTCTGCGTTCAGGATCACGGGGCTTCTTGC  
TTAGCTTGGGCATCCACCTAAATGCTGCTGCAAAATACACATCTTTTCTTGGCTCCTTAATGCGCGCTAG  
GTTTTATGCTGCTGAGTCTGCTAGTACCTTTCAATGCGGCTTTCCACATTGCCCTAGCTTTTAGCTATATGAA  
GCTGCTTTAGTCTGACTTTTACAGTTTAGCAGAGGAGCAATCCTGCTGCTATGTCTGATATTCTTCTTAA  
ACGCAGCAGCCACACACTCTGAAAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGGGGACC  
40 CAGCCTCTACAAAGCATACCCTGCCCTGATGCCACTATACGCATGCATTGGCGCGCAGCCTGGTTATCCCTT  
TTAGTACCGTTTGTCAACTTTCTATTAAACCAAGATCTGACGATTAATATTCGATCCCAAGTTCTTGGGCAT  
TCAAAGCAGCCGCGAGTATCTGGTTTCAATTGGCGTATGGAACCTGCCAAGCGACTTCTTCTCTGTTAA  
GTTCTCTCCCTCCGATTTCTTTCCATCGGTGAAAGACCTCCTTGATACCGCGAGCGCTCTGTACAACTCGTGG  
CCAAAATTCGAGTTCCAAACCTAAAGCCGCCAGTGCCATTGTTCCGTGGTAAAGAGAAAATTATCAC  
45 TCGACGTGTCCGAGCATTTTATAACGCTGCTGCAAGTTTGTGCGAGCATGGACATTGAAGGCTGCAGCGAA  
AGCAGCAAATGTATCAATACCCTGGACCCACAAAGGTGACGCCGGCTGTCTAGGTATGTGGCGAGGCTAAAC  
GCCGCCGCTCAACACTGCCCTGAGACTACTGTGCTGAGACGCAACACCCCTGCCGCAATGCCCCACCTCTGA  
AAGCAGCCGACGATGGATGTGCGCTCAGAAGATTCATAAAGCCTTCTTTCTGTGGTCAACCTACAAAGC  
CGCTTACATGGACGATGTGGTCTCGGAGTGAATGCCCTCTGGTTCCATATCAGCTGCCGTGACATTCAAGGCA  
50 GCCGCCACCCCGCTCGTGTGACAGGAGGTCTTCAAAGCCGCGGCACTGACTTTGGTGGGAAACTGTAT  
TGGAATATAAGCAGGCTTACATTCTCCCAACATACAAGTGA

**Figure 23A**

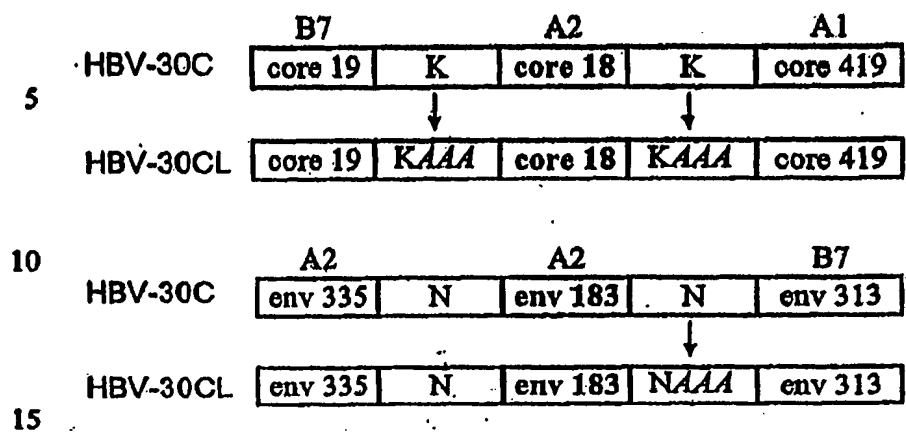




Figure 23B

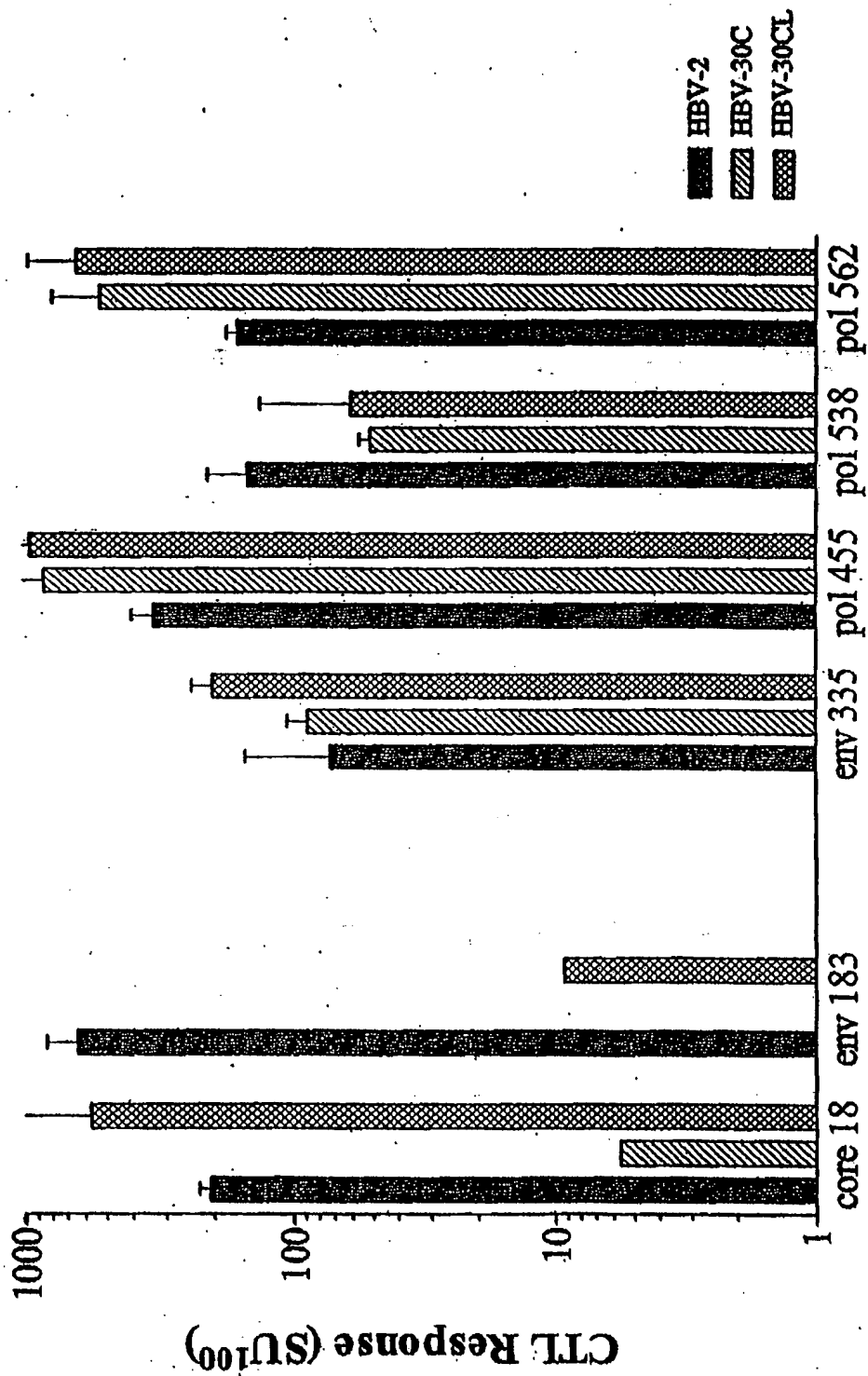


Figure 23C

HBV-CL

5    MQVQIQSLFLLLLNWPGSRGFLLSLGIHLNAAAKYTSFPWLLNAAARFSLSLVLPFNAAFPHCLAYSYMKAA  
    LVVDFSQFSGAILLLCLIFLLNAAHTLWKAGILYKKAWMMWYWGPSLYKAYPALMPLYACIGAAWLSLLV  
    PFVNFL/TRLITINAAAIPIBSSWAFKAAAEYLVSFGVWNLPSDFPFSVKAAAFPSDFPFSVKAAADLLDTA  
    SALYNSWPKFAVENLKAAAASAICSVVRKLSLDVSAAFYNAAAKFVAATLKAARAKAANVSIPTWTHKGAAGLS  
    RYVARLNAAASTLPBTTTVVRKHFAAMPHLKAAARWMCLRRFIINASFCGSPYKAAAYMDDVVLGVNALWFHI  
    SCLTFKAAATPARVTGGVFKAALTFGRETVLEYKQAPTFSPTYK

10    ATGGGAATGCAGGTGCAAATACAGTCTCTCTTCTTTCTTCTCTGGGTTCAGGATCACGGGGCTTCTTGC  
    TTAGCTTGGGCATCCACCTAAATGCTGCTGCAAAATACACATCTTTCTTGGCTCCTTAATGCCGCCGCTAG  
    GTTTTCATGGCTGAGTCTGCTAGTACCTTTCAATGCGGCTTTCCACATTCCTAGCTTTTAGCTATATGAAA  
    GCTGCTTTAGTCGTGGACTTTTACAGTTTAGCAGAGGAGCAATCCTGCTGCTATGTCTGATATTCTTCTAA  
    ACGCAGCAGCCACACACTCTGGAAAGCTGGTATCCTTTACAAGAAAGCCTGGATGATGTGGTATTGGGGACC  
    CAGCCTCTACAAAGCATAACCTGCGCTGATGCCACTATACGCATGCATTGGCGCGGCAGCCTGGTTATCCCTT

15    TTAGTACCGTTTGTCAACTTTCTATTAAACCAGAATCCTGACGATTAATGCTGCCGCCATTCCGATCCCAAGTT  
    CCTGGGCATTCAAAGCAGCCGCGGAGTATCTGGTTTCATTGCGGTATGGAACCTGCCAAGCGACTTCTTTCC  
    TTCTGTTAAGGCCGCTGCTTTCTCCCTCCGATTTCTTTCCATCGGTGAAAGCCGCTGCCGACCTCCTTGAT  
    ACCGCGAGCGCTCTGTACAACCTCGTGCCAAAATTTCGAGTTCCAAACCTAAAAGCCGCCCGCAGTGCCATT  
    GTTCCGTGGTAAGGAGAAAATTATCACTCGACGTGTCCGCAGCATTTTATAACGCTGCTGCAAAGTTTGTCCG

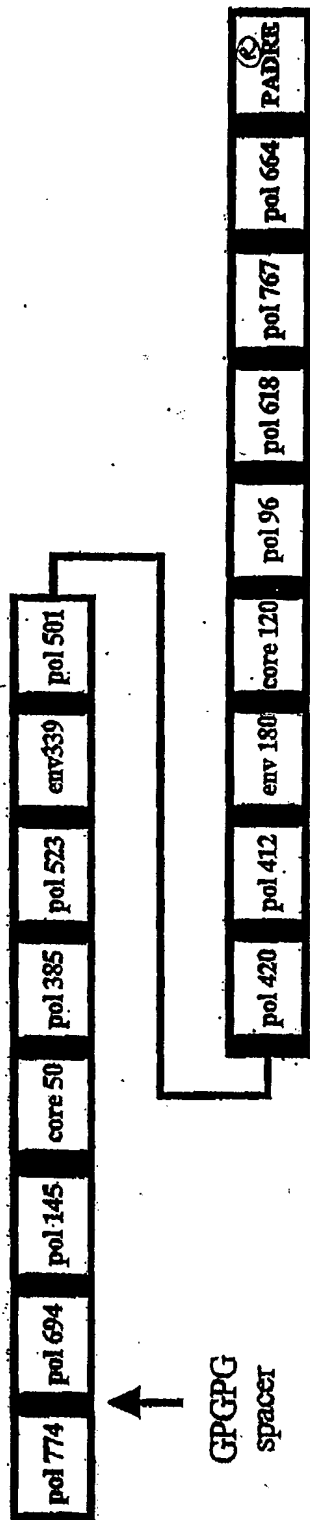
20    AGCATGGACATTGAAGGCTGCAGCGAAAGCAGCAATGTATCAATACCTGGACCCACAAGGGTGAGCCGGG  
    CTGTCTAGGTATGTGGCGAGGCTAAACGCCGCCCTCAACACTGCCTGAGACTACTGTCTGTGAGACGCAAC  
    ACCCTGCCGCAATGCCCCACCTGCTGAAAGCAGCCGCACGATGGATGTGCTCAGAAGATTATAATAAACGC  
    TTCTTTCTGTGGTCAACCTACAAAGCCGCTTACATGGACGATGTGGTCTCTCGAGTGAATGCCCTCTGGTTC

25    CATATCAGCTGCCGACATTCAAGGCAGCCGCCACCCGCTCGTGTGACAGGAGGTGTCTTCAAAGCCGCCG  
    CACTGACTTTCGTCGGGAAACTGTATTGGAATATAAGCAGGCCTTCACATTCTCCCCAACATACAAGTGA

Figure 24A

Sample	Depth	SOL	PLAOK Group Counts (C20-PA)															
			DR1000	DR1001	DR1002	DR1003	DR1004	DR1005	DR1006	DR1007	DR1008	DR1009	DR1010	DR1011	DR1012	DR1013	DR1014	DR1015
DR	pd 412	10	210	21	-	1010	47	303	387	143	173	698	761	1087	1837	4179		
	pd 414	41	10	41	-	88	101	62	-	190	90	416	142	144	4848	322		
	pd 416	10	1	217	-	9	226	6	4229	9	8	189	65	1183	4374	898		
	pd 418	9	15	748	-	119	94	443	-	-	94	818	220	400	-	-		
	pd 420	8	27	45	-	53	220	11	817	683	73	78	1773	7	8454	396		
	pd 422	10	17	4.0	-	2271	1109	42	149	788	61	38	133	35	-	782		
	pd 424	9	408	14	-	315	28	54	482	2330	2744	60	31	1816	1681	22		
	pd 426	8	248	598	-	77	244	482	9462	-	-	300	1551	660	-	102		
	pd 428	7	27	359	-	593	248	1749	-	59	328	940	1573	4784	-	1947		
	pd 430	6	3.0	4370	-	40	34	1817	-	821	62	872	5178	1248	-	3080		
	pd 432	8	55	308	-	988	1834	1820	802	143	44	214	299	3278	-	6553		
	pd 434	7	810	3.0	-	28	-	451	-	-	679	210	852	124	575	48		
	pd 436	2	7470	5009	67	480	1203	-	-	2022	-	-	-	-	1808	1044		
	pd 438	3	7372	1398	39	205	231	-	-	948	-	-	-	-	2525	8711		
	pd 440	1	8475	4153	43	3918	7808	8888	-	4481	-	5354	-	4330	-	8121		
	pd 442	4	35	5059	62	185	17	4523	1853	38	8083	1085	7128	-	8	7		

Figure 24B



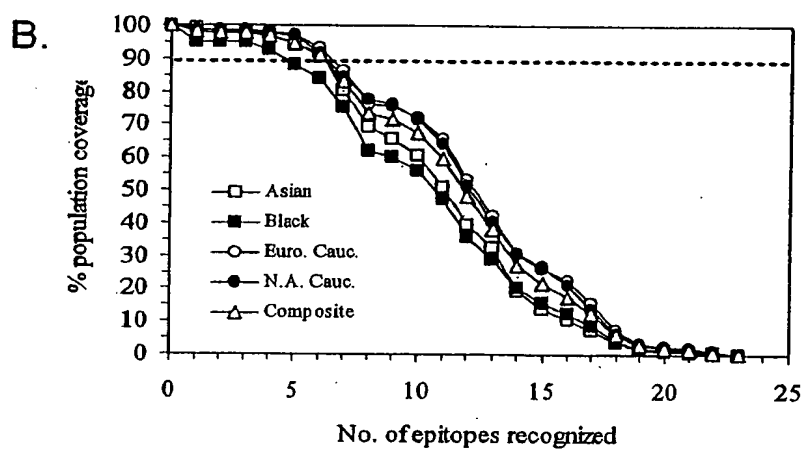
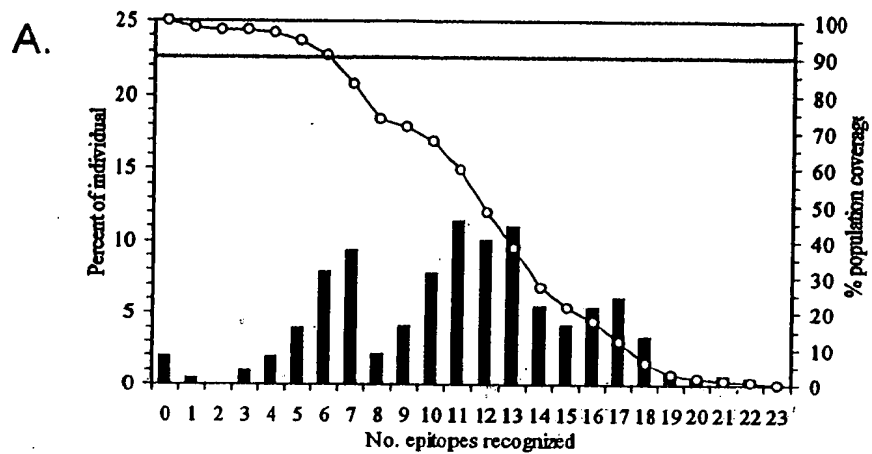
GPGPG  
spacer

Figure 24C

HBV-HTL

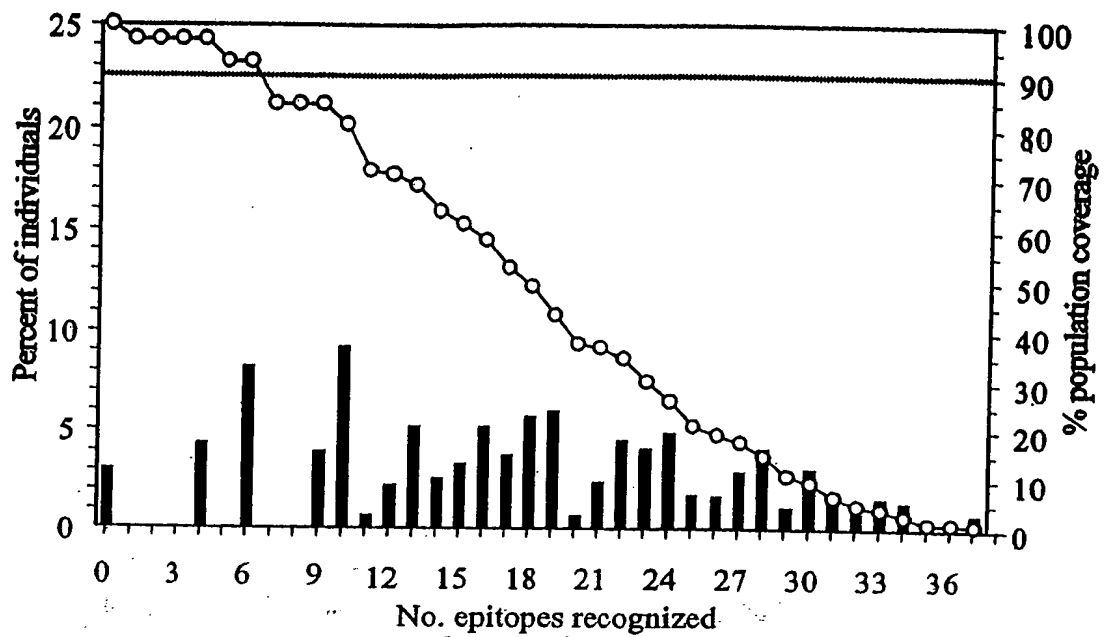
5 MGTSTFVYVPSALNPADGGPGGLCQVFADATFTGWGLGPGPGRHYLHTLWKAGILYKGPQPGPHHTALRQAILC  
WGLMTLAGPGPGESRLVVDTSQFSRGNGPGPGPFLLAQFTSAICBVVGPGLVPPVQWVGLSPTVGPQPG  
LHLYSHPIILGFRKIQPGPGSSNLNLSLDVSAAFQPGPGQLQSLTNLLSSNLNLSWLGPGPGAGFFLLTRILTIP  
QSGPGPGVSGVWIRTPPAYRPPNAPIGPGPGVGLTVNEKRRLKLIGPGPGKQCFRKLPNRPIDWGPGPGA  
ANWILRGTSFVYVPGPGPGKQAFTFSTYKAFLCGPGPGAKFVAAWTLKAAA

10 ATGGGAACCTTCTTTTGTGTATGTCCCTTCGGCTCTGAACCCAGCAGACGGACCCGGGCTGGCCTGTGCCAGG  
TCTTC3CCGACGCAACTCCACAGGGTGGGGGCTGGGGCCAGGACCAGGCAGGCACTACCTGCATACTCTGTG  
GAAGGCAGGAATCCTCTATAAGGGCCCGGCCAGGCCCTCACCACACCGCCCTGAGGCAGGCCATCCTGTGC  
TGGGGGGAGCTCATGACCTGGCCCGACCTGGACCCGGGAGAGCAGACTGGTGGTGGATTTAGCCAATTCA  
GCAGAGGAAACGGACCCGGCCCTGGGCTTTTCTGCTGGCTCAGTTTACATCTGCTATTTGTTCTGTGGTCGG  
CCCGGGCCCGGACTCGTGCTTTCTGTGAGTGGTTCTGTGGGACTGTCCCTACAGTCGGGCGCCGGCCAGGG  
15 CTGCATCTGTACTCCCAACCAATCATGCTGGCTTCCGCAAGATTGGACCCGGCCAGGCTCCAGCAATCTCT  
CCTGGCTCTCTCTGGACGTGTCTGCGCCCTTGGCCCTGGACAGGCCCTGCAAGCCTGACTAATCTGCTCAG  
CAGCAACCTGTCTGGCTGGGACCTGGCCCGGGGCTGGCTTCTTTCTGCTCACCCTGATTCTCACAATTCCC  
CAGTCCGGACAGGACAGGAGTCAGTTTCGGGGTGTGGATCAGGACCCCTCCTGCTTATAGACCACCAATG  
CTCCAATCGGCCCGGCCCTGGCGTCCGGCCACTGACCGTGAATGAGAAGCGCGGCTGAAGCTGATCGGCCC  
20 TGGCCCTGGCAAGCAGTGTCTTTCGCAAACTGCCCGTGAACAGACCTATTGATTGGGGCCCCGGCCCTGGAGCA  
GCCAACTGGATTCTCAGGGGAACAAGCTTCGTCTACGTGCCCGGGCCCGGACAGGGAAGCAGGCTTTTACCT  
TCTCTCCCACTTACAAGGCCTTCTCTGTGGGCCAGGCCCGGCGCAAGTTTGTGGCAGCATGGACCCTCAA  
AGCCGCTGCCTGA

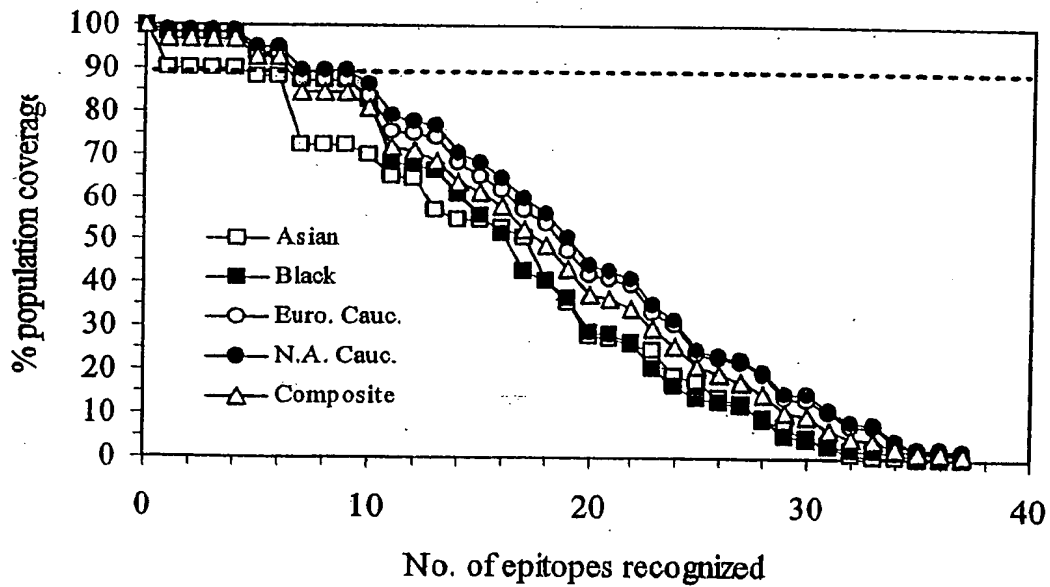


**Figures 25A-B**

A.

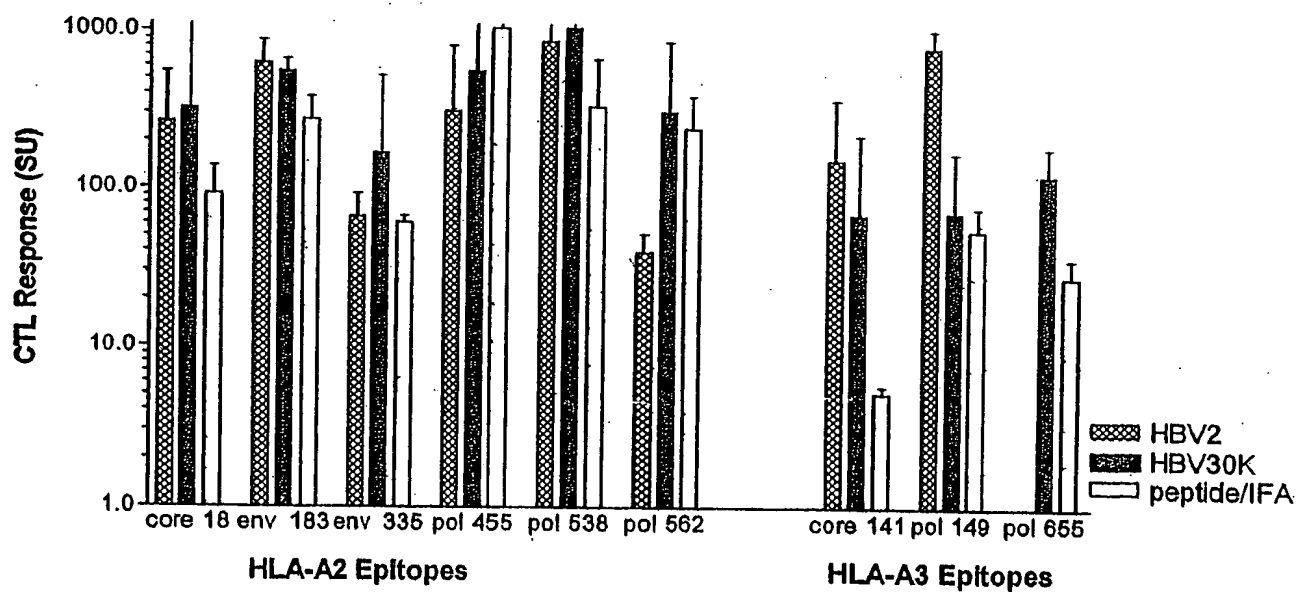
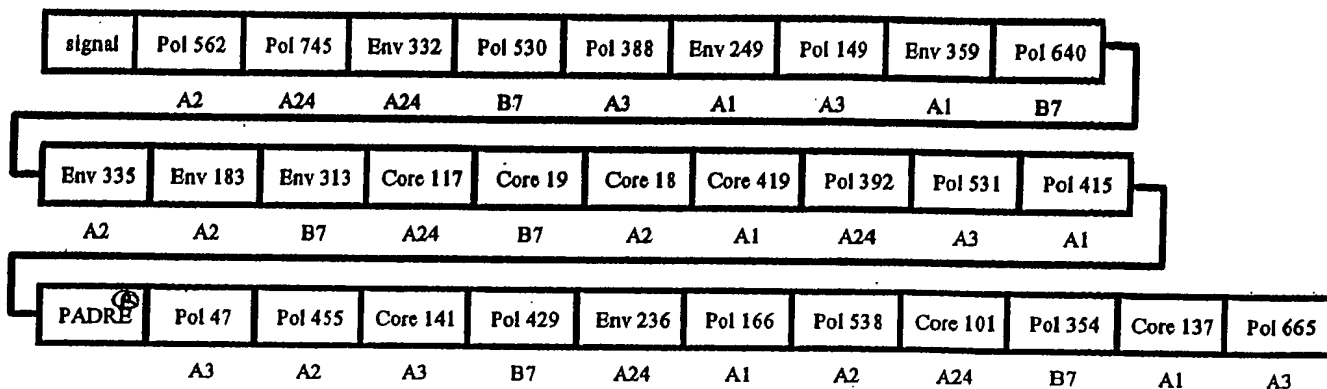


B.



Figures 26A-B

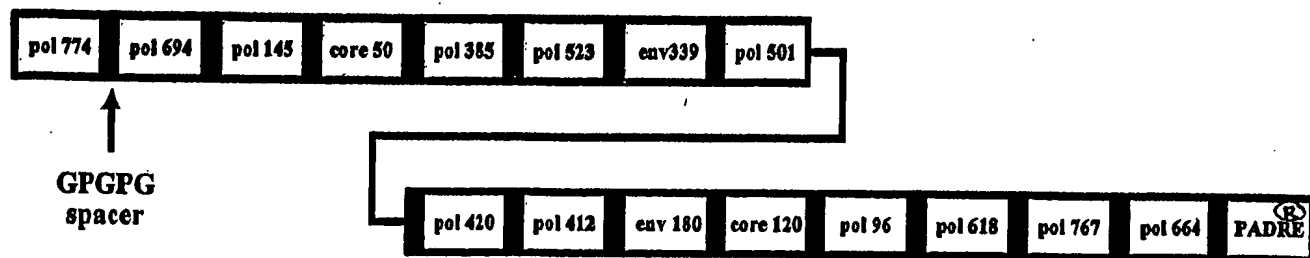
A.



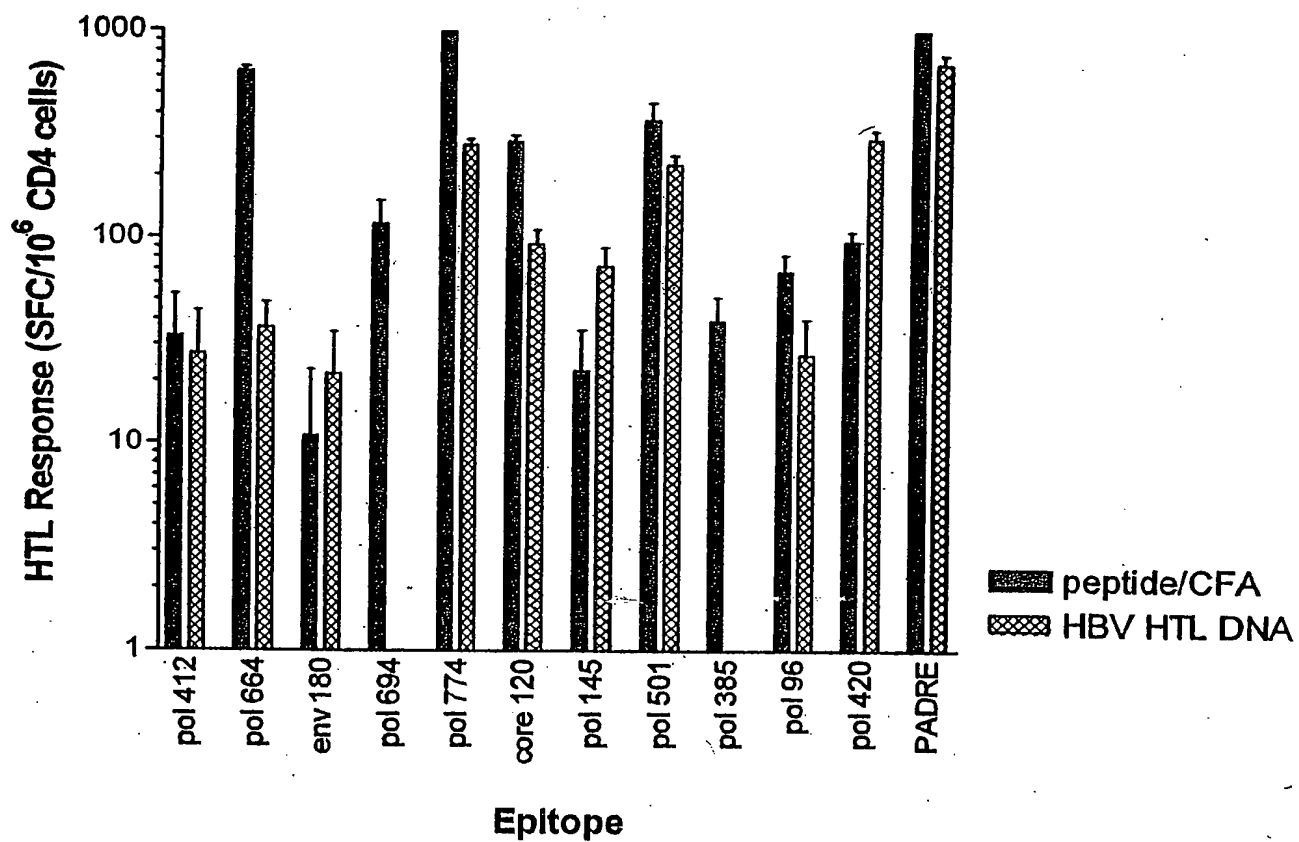
Figures 27A-B



A.

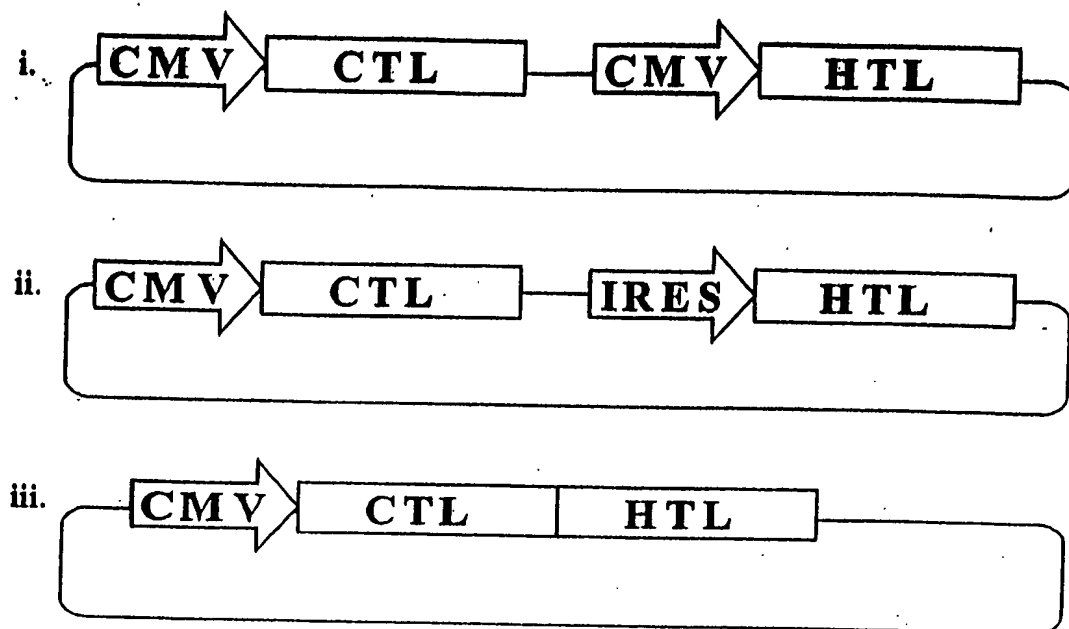


B.

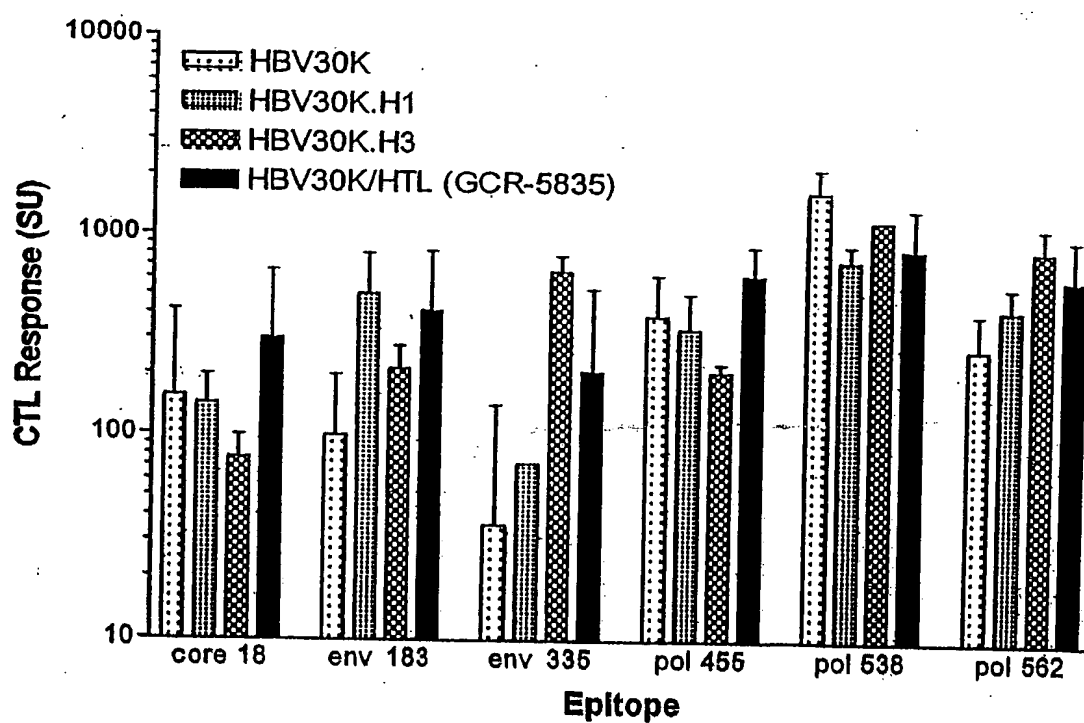


Figures 28A-B

A.



B.



Figures 29A-B

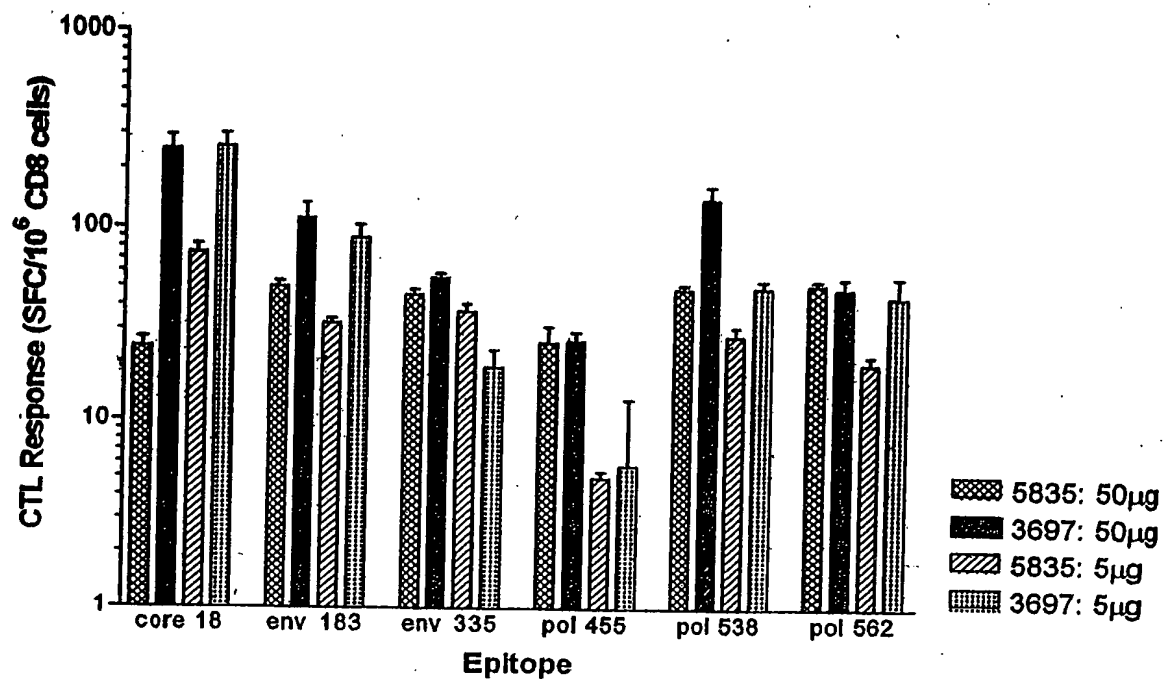
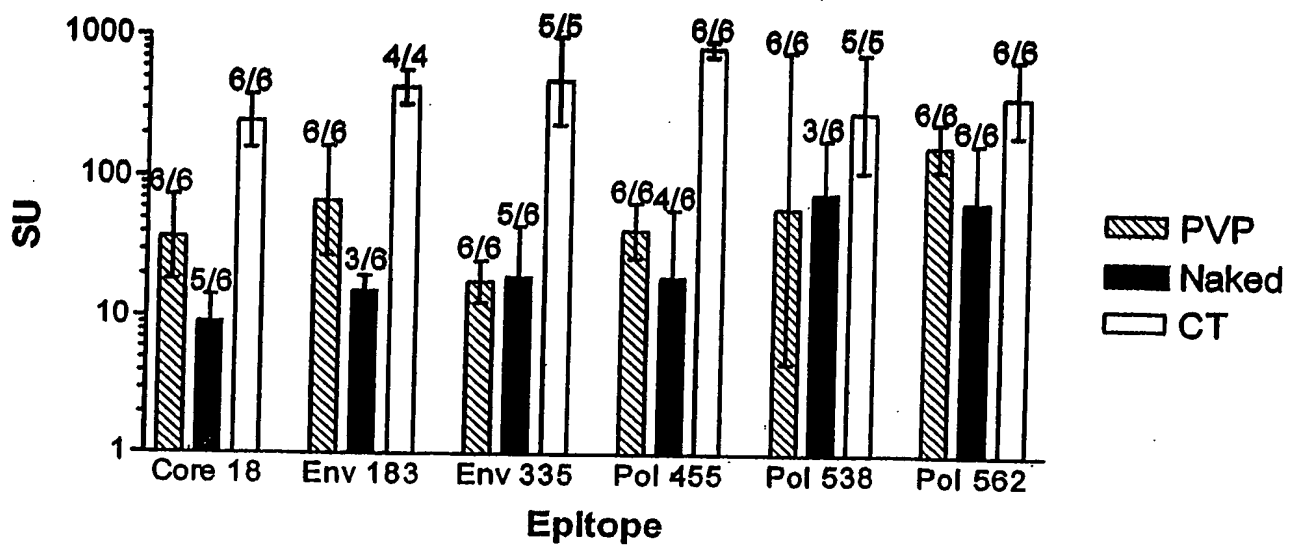
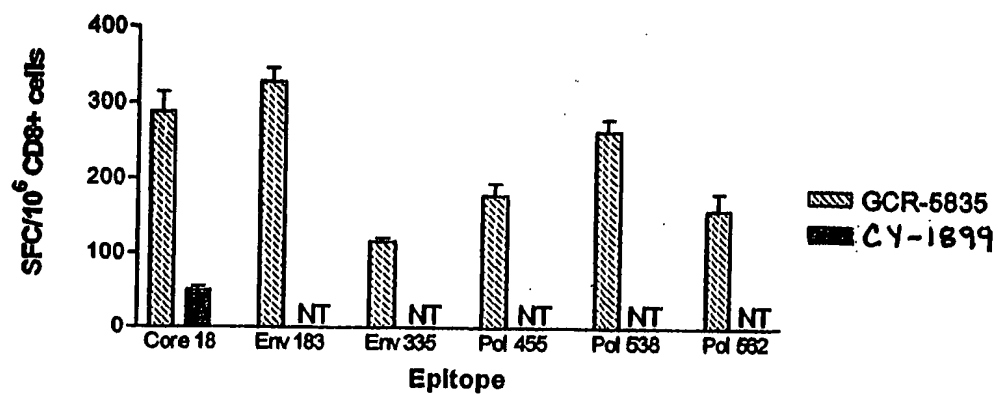


Figure 30

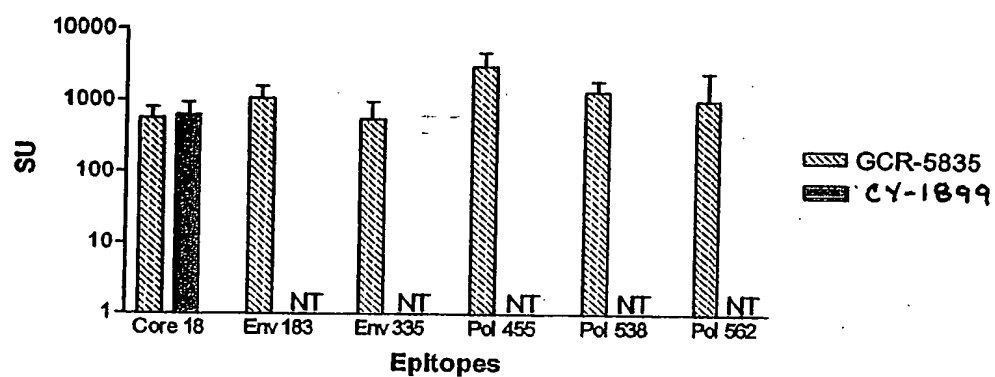


**Figure 31**

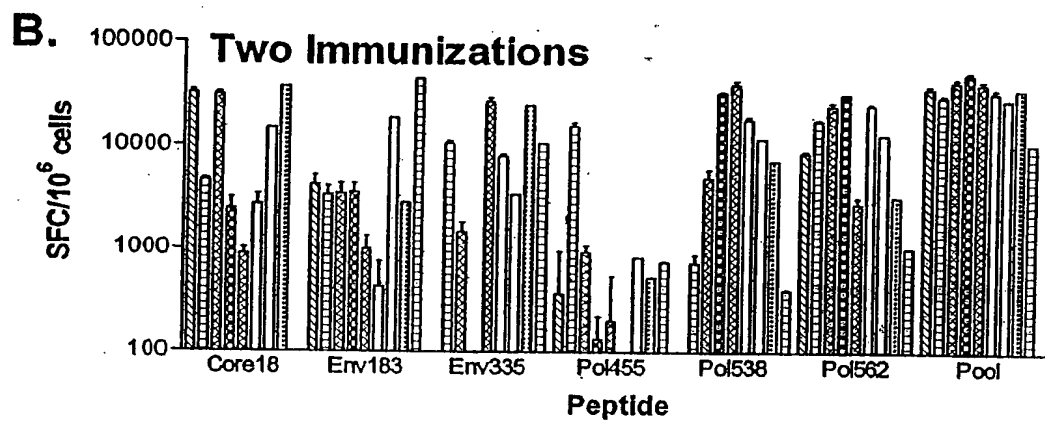
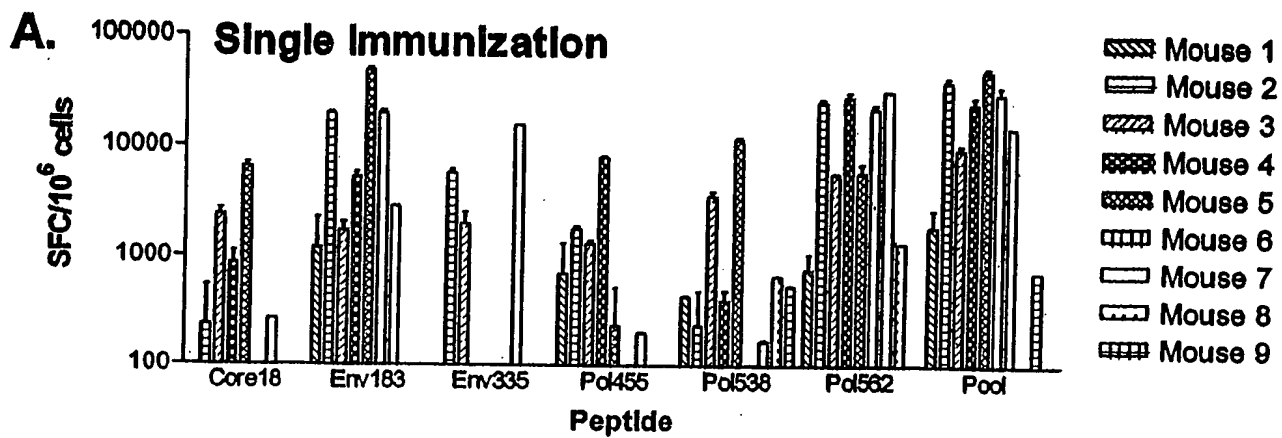
**A.**



**B.**



**Figures 32A-B**



Figures 33A-B

# Composition of HBV poly-epitope vaccine

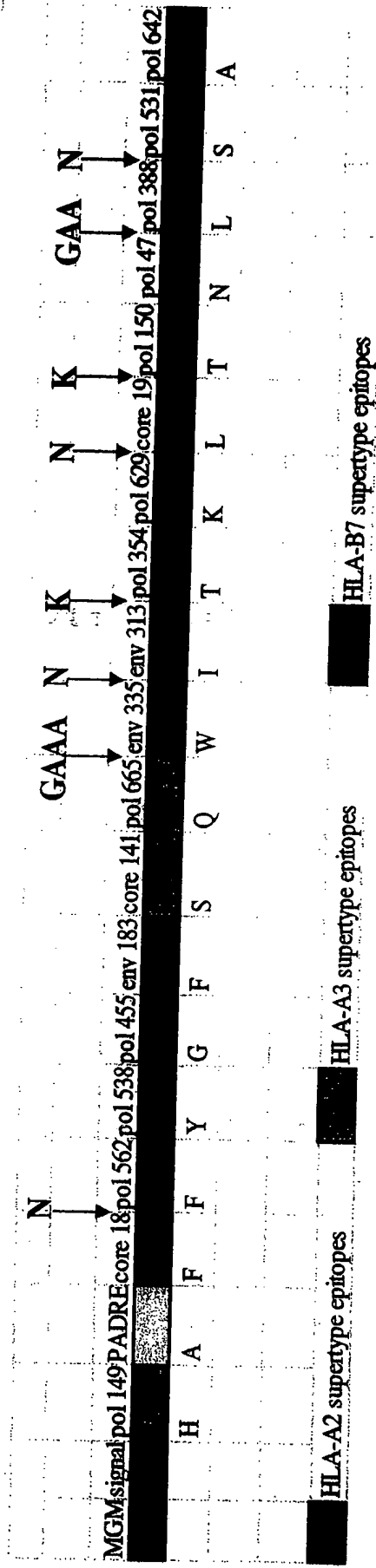
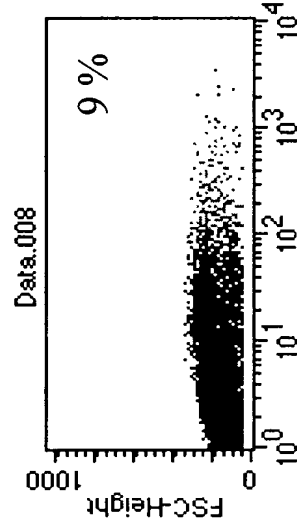
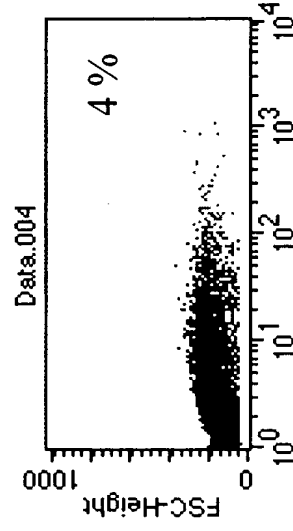
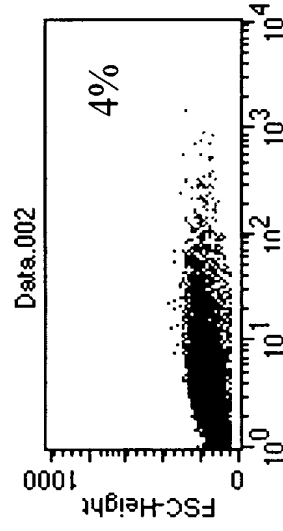
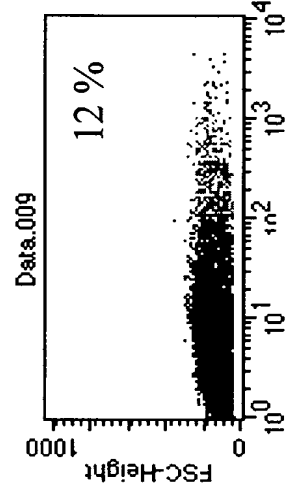
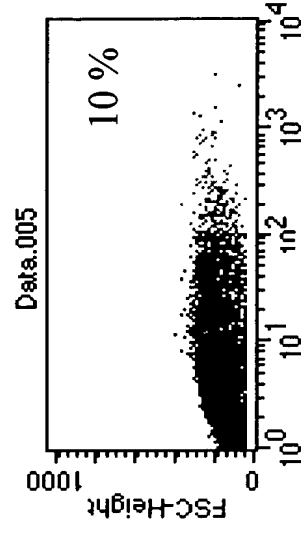
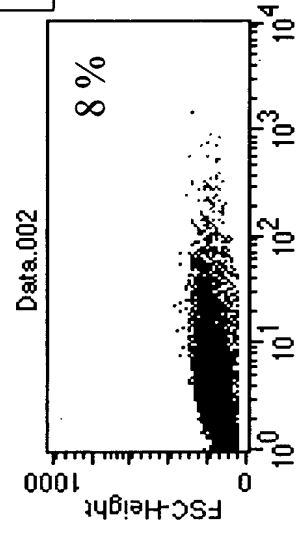


FIG. 34

No inhibitor



+ MG132



Incubation period in  
presence of inhibitor

0 hrs

2 hrs

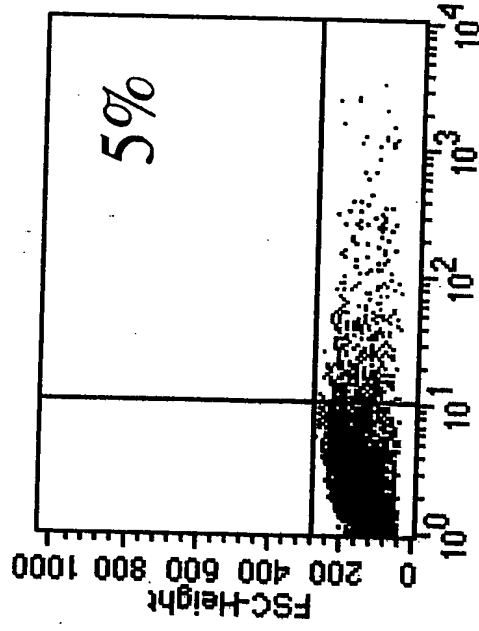
16 hrs

FIG. 35 A



# Detection of HBV AOSIb (un-optimized epitope string)

- MG132



+ MG132

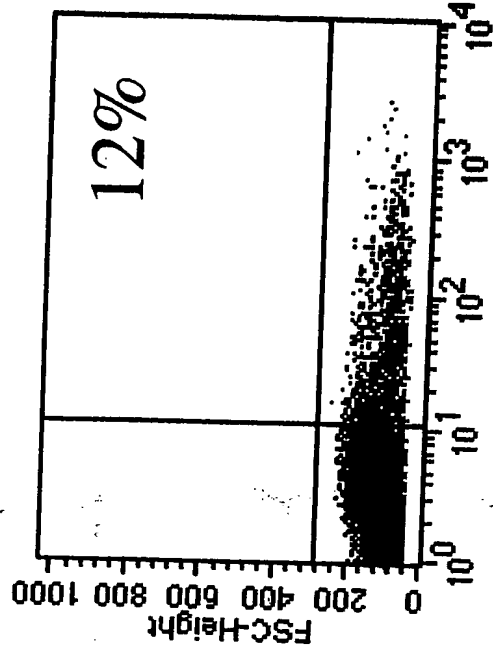
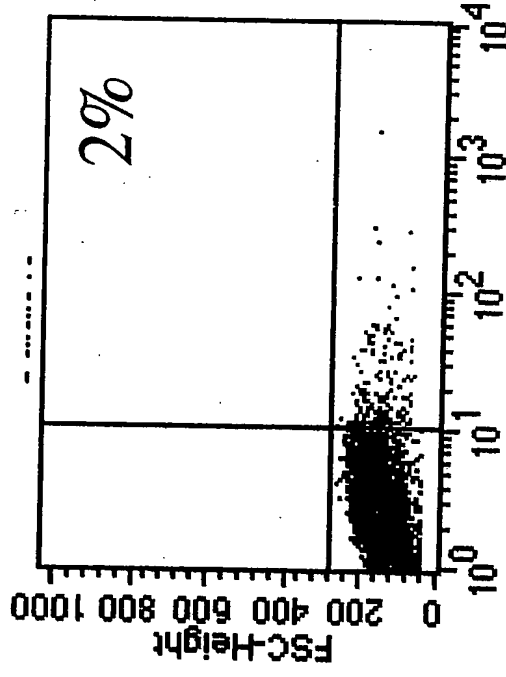


FIG. 35B

# Detection of HBV AOSIb2 (processing optimized epitope string)

- MG132



+ MG132

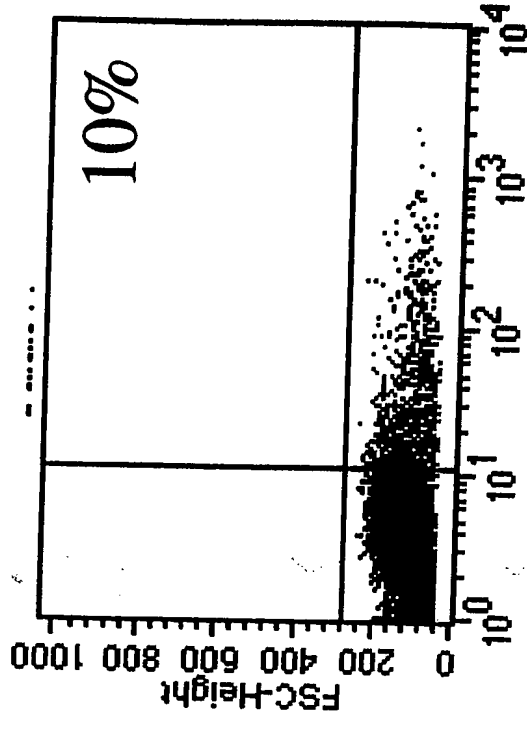


FIG.35C

## Comparison of fluorescence intensity

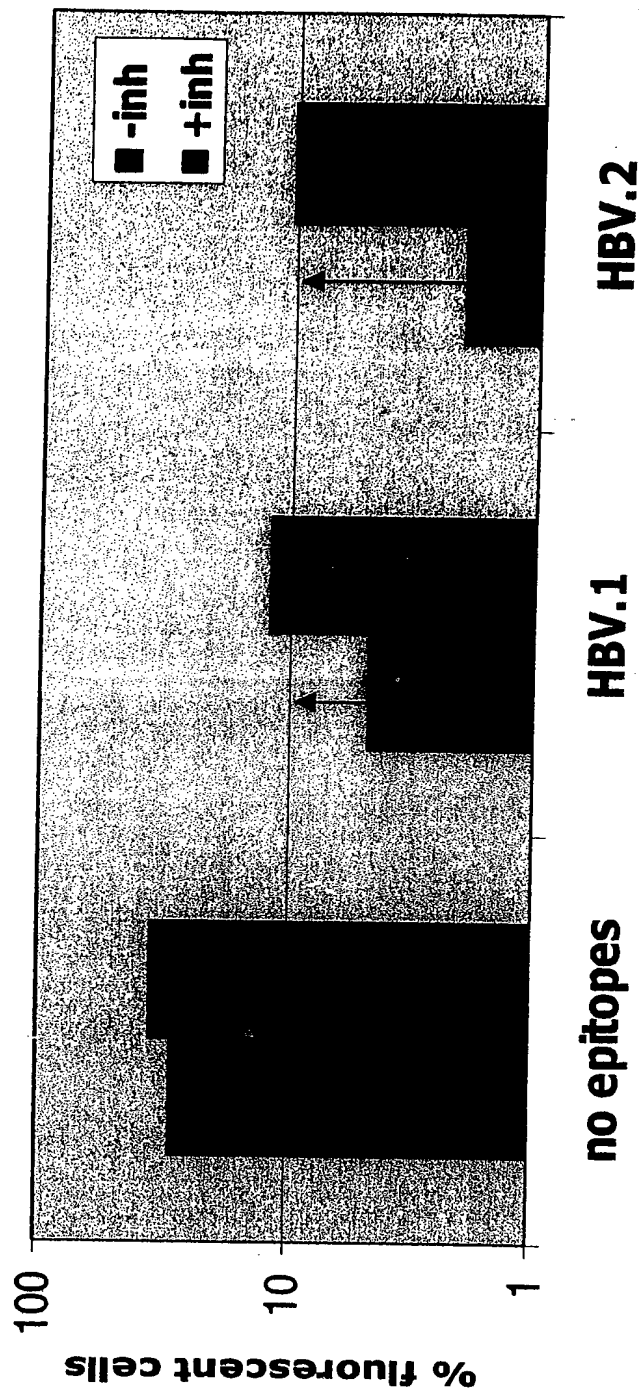


FIG. 35D

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<b>plasmid</b>	<b>No inhibitor</b>	<b>with inhibitor</b>	<b>Fold Increase (aver.)</b>
Fluorescent Protein (no epitopes control)	30% 34%	35% 33%	1.1
HBV AOSIb fusion	5% 4.4	12% 8%	2.1
HBV AOSIb2 fusion	2% 1.2%	10% 6.6	5.3

FIG. 35E

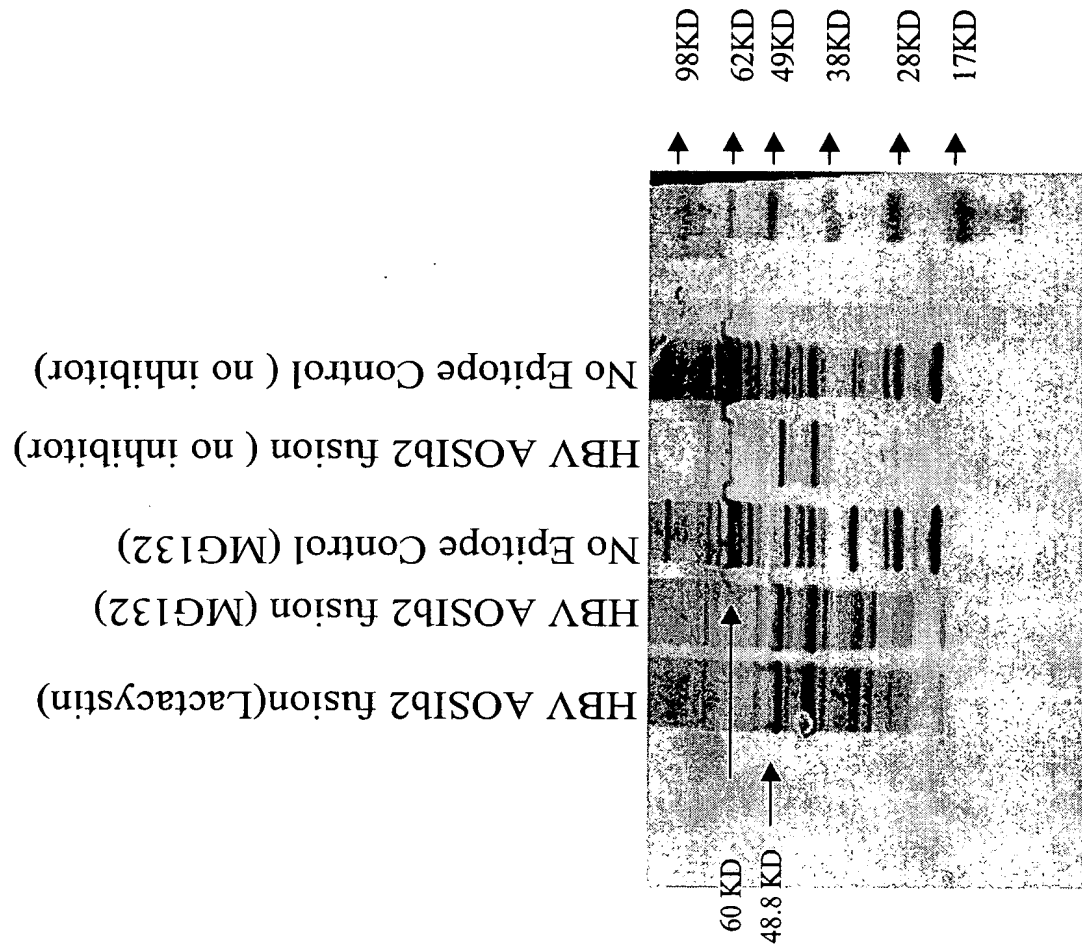
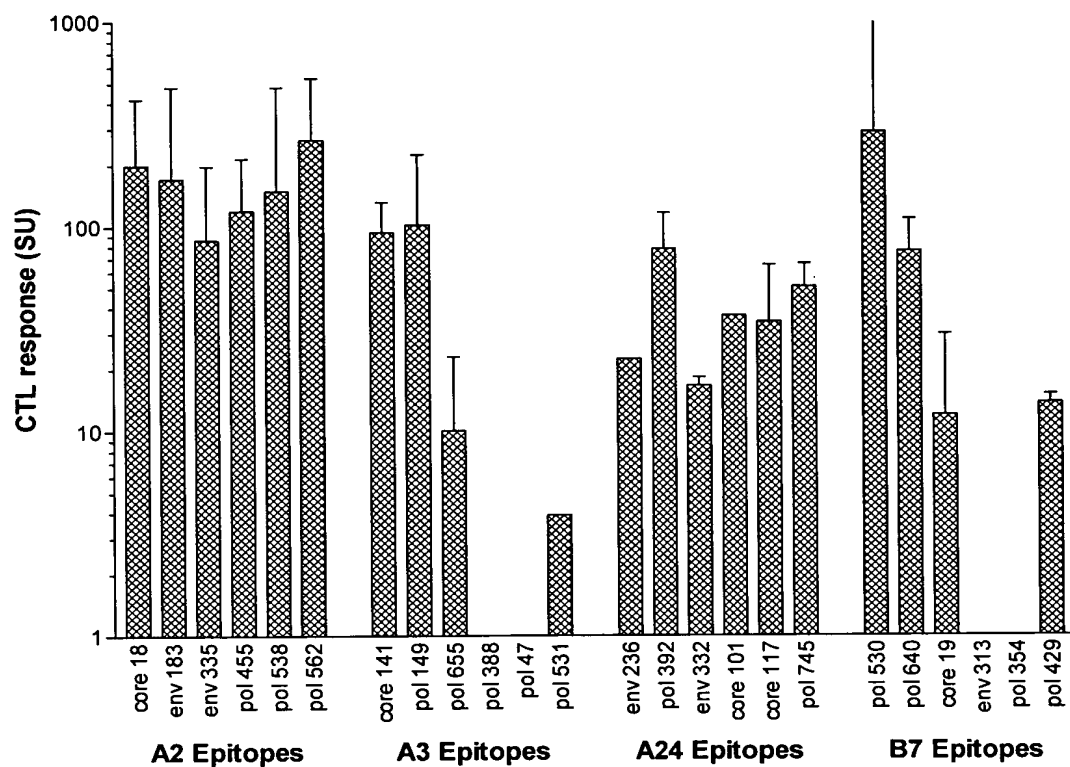


FIG. 36

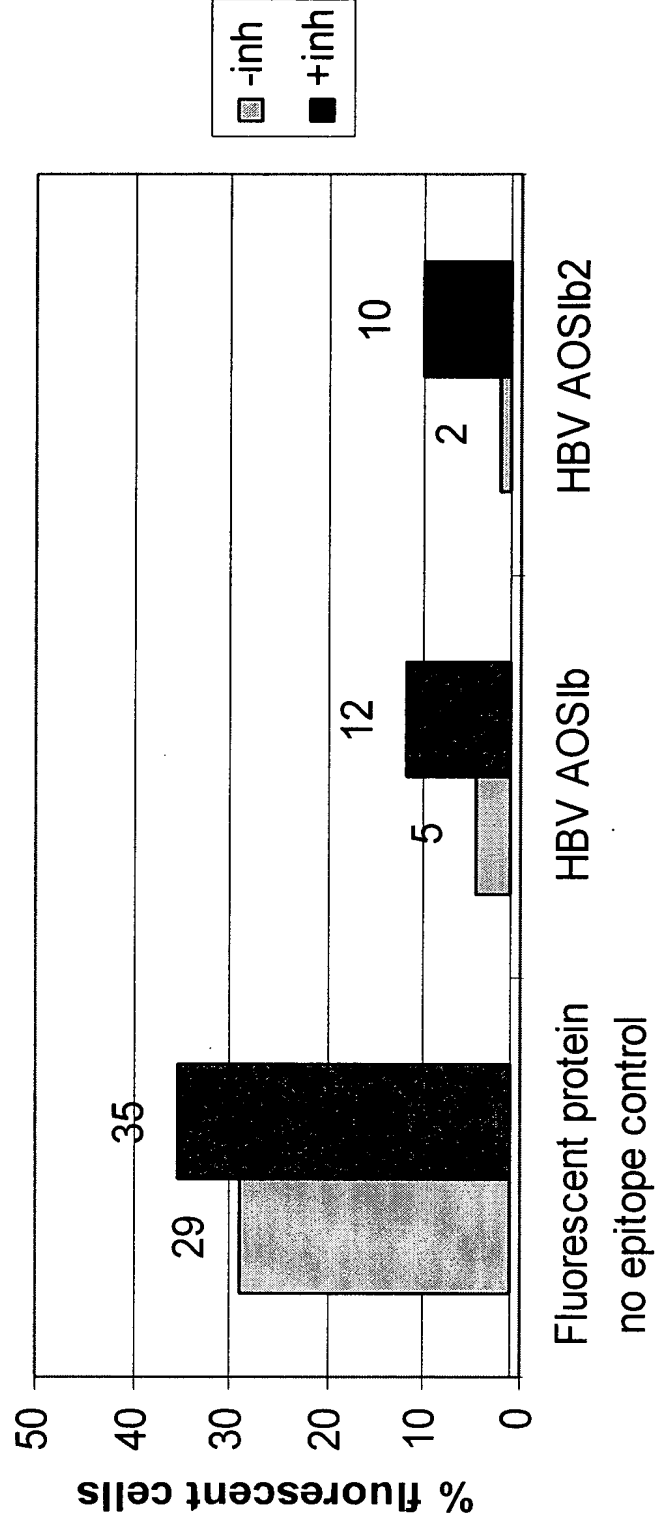


### GCR-3697 Immunogenicity Data

HLA Supertype	Epitope	CTL response (SU)					
		2 x PVP Immunization			CT Pre-treatment		
		Freq.	GeoMean	X/+	Freq.	GeoMean	X/+
HLA-A2	core 18	12/12	199.3	2.1	4/4	288.9	1.3
	env 183	12/12	171.2	2.8	4/4	401.2	1.4
	env 335	12/12	86.4	2.3	4/4	153.6	1.7
	pol 455	12/12	120.4	1.8	4/4	411.3	1.8
	pol 538	12/12	149.9	3.2	4/4	148.1	2.2
	pol 562	12/12	266.2	2	4/4	353.3	1.5
HLA-A3	core 141	6/6	94.4	1.4	12/12	167.6	1.4
	pol 149	6/6	103	2.2	12/12	386.7	1.5
	pol 655	5/6	10.1	2.3	12/12	108	3.6
	pol 388	0/6			0/12		
	pol 47	0/6			3/12	3.2	1.1
	pol 531	1/6	3.9		2/12	5.5	1
HLA-A24	env 236	1/6	22.6		2/11	23.4	1.2
	pol 392	5/6	78.1	1.5	10/11	54.8	2.2
	env 332	2/6	16.7	1.1	3/11	25.6	1.6
	core 101	1/6	37		0/11		
	core 117	3/6	34.4	1.9	2/11	27.4	3
	pol 745	2/6	51.2	1.3	1/11	32.6	
HLA-B7	pol 530	6/6	292.4	3.1	3/6	177	1.3
	pol 640	4/6	76.5	1.7	5/7	104.6	1.8
	core 19	3/6	12	2.5	2/7	8.8	1.6
	env 313	0/6	0	0	6/6	323.1	2.9
	pol 354	0/6	0	0	4/6	351.5	3.2
	pol 429	2/6	13.7	1.1	1/6	1.4	

FIGURES 37A-37B

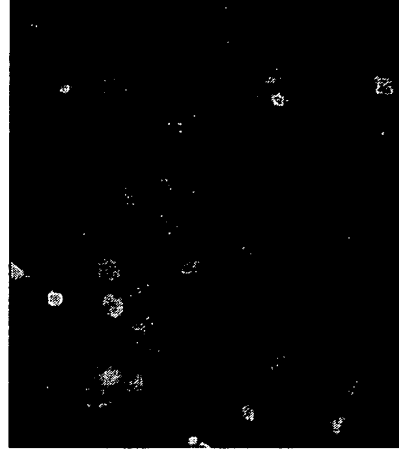
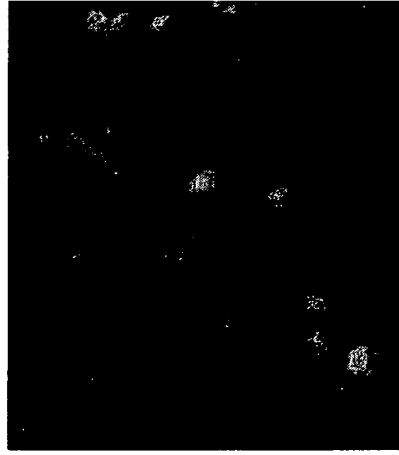
**Comparison of fluorescent cell number as determined by  
FACS**



**FIG. 38**

No Inhibitor

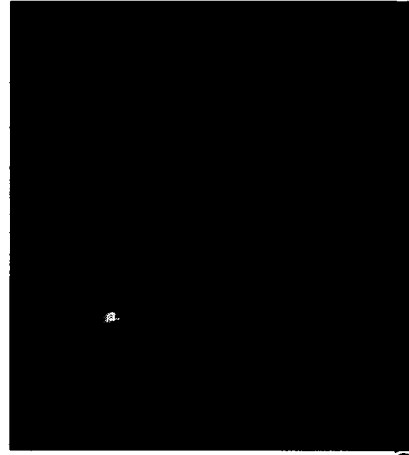
+MG 132



Fluorescent protein no  
epitope control



HBV AOSIb



HBV AOSIb2

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FIG. 39